

STIC-Biotech/ChemLib

79094

From: Portner, Ginny
Sent: Wednesday, October 30, 2002 3:18 PM
To: STIC-Biotech/ChemLib
Subject: priority search

Importance: High

Please search the sequences in Application 09/910,186 against 08/123,975; 60146,192; 60/133,866;
60/133868; 60/133869; 60/133,865; 60133,873 and 60/133,867. Thanks

Ginny Portner
CM1, Art Unit 1645
Room 7e13
Mail box 7e12
(703) 308-7543

Ginny,
None of the provisional cases have CRF's, so
I could only compare ① with ②.
Barb

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

RECEIVED
OCT 30 2002
STIC

Searcher: BoB
Phone: _____
Location: _____
Date Picked Up: 11-7
Date Completed: 11-7-02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: 1

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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TCTGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGC
1190 1200 1210 1220 1230 1240 1250
1250 1260 1270 1280 1290 1300 1310 1320
GAACGTTCCCTCTCGGCACTCTGGTTCCTCTTCGGAGTTCATCCCGGTTGATGACGGTTGGGTGAACGTCGG
1111 1111 1111 1111 1111 1111 1111 1111
AAACCGTACAACCTGAACCTGGTTGCAATTGGCAGTTTCATCCCGAAAGACGAAGGTTGGACCCGAATAGTAA
1260 1270 1280 1290 1300 1310 1320
1330 X
CTGTAAGAATTC
1111111
CCTCTAGAGTCGAGGCGCTCCAG
1330 1340 1350

```



```
1200 1210 1220 1230 1240 1250
AACGATGTGATTT--TCGAACCGTAGCGACAGTCGATCAGGTGATTGGATTCTGACCGCAGGT-----
|||||
TAACGATTCGGTTTCATCGGTTCCACCGATTCAACAATATCGTAACTGGTGTCTTCCAACGTGTACAA
1170 1180 1190 1200 1210 1220 1230
1260 1270 1280 1290 1300 1310 1320
---TCAGGATGGAGGTATTGATGATTTCT---TTGATGATTTCAGTGAAGGTAGACAGCAGACGCATCGTT
|||||
TCGTCAGATCGAACGTTCCTCTCGCACCTCGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGG
1240 1250 1260 1270 1280 1290 1300 1310
1330 X
TCGAATTC
| | |
TGAACGTCGCTGTAAACCGGGAAGCT
310 1320 1330
```

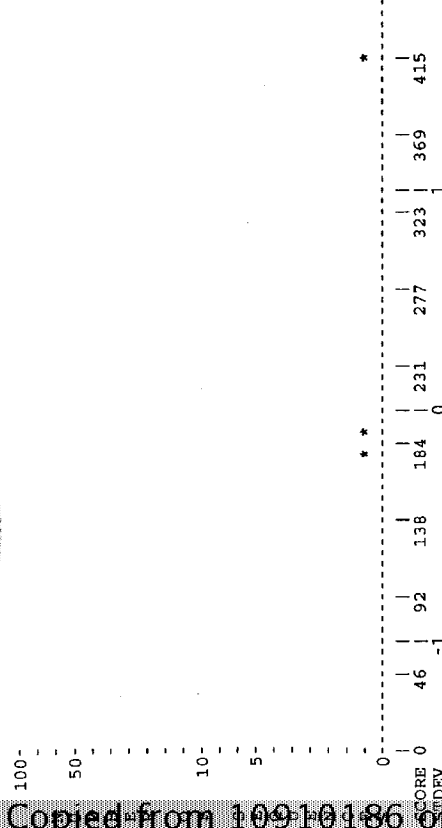
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-2.res made by bobryen on Thu 7 Nov 102 14:31:34-PST.

Query sequence being compared: US-09-910-186A-2 (1-437)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-2 (1-437) with:
File : US08123975A.pep



PARAMETERS

Similarity matrix PAM-150
Threshold level of sim. 16%
Mismatch penalty 1
Gap penalty 5.00
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 262 Median 181 Standard Deviation 132.08
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Frame
1. US-08-123-975A-3	Sequence 3, Application U	415	415	1.16	0
2. US-08-123-975A-5	Sequence 5, Application U	439	273	-0.52	0
3. US-08-123-975A-2	Sequence 2, Application U	850	180	275	-0.62

1. US-09-910-186A-2 (1-437)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score = 415
Residue Identity = 100%
Gaps = 0
Optimized Score = 415
Matches = 415
Conservative Substitutions = 0
Significance = 1.16

10 20 X 30 40 50 60 70
LLSTFTEYIKNIINTSILNRYESNHLIDLSRYASKINIGSKYVNFDPIDKNQIQLFNLESSKIEVILKNAIV
RYESNHLIDLSRYASKINIGSKYVNFDPIDKNQIQLFNLESSKIEVILKNAIV
X 10 20 30 40 50

80 90 100 110 120 130 140
YNSMYENFSTFWIRIPKYNFNSISLNNEYTIINCWENNSGKYSVNLVGEIITWLTQTOETKORVVFYKYSQMI
YNSMYENFSTFWIRIPKYNFNSISLNNEYTIINCWENNSGKYSVNLVGEIITWLTQTOETKORVVFYKYSQMI
X 70 80 90 100 110 120

150 160 170 180 190 200 210
NISDYINRWIFVTITNRLNNSKIYINGRLIDOKPISNLGNIHASNNIMEKLDGCRDTHRYIKYFNFLFDK
NISDYINRWIFVTITNRLNNSKIYINGRLIDOKPISNLGNIHASNNIMEKLDGCRDTHRYIKYFNFLFDK
X 130 140 150 160 170 180 190

220 230 240 250 260 270 280 290
ELNEKEIKDLYDNOSGILKDFGDLQYDKPYMLNLYDPNKYVDNVNNGYMLKPGSGSVMTNIIY
ELNEKEIKDLYDNOSGILKDFGDLQYDKPYMLNLYDPNKYVDNVNNGYMLKPGSGSVMTNIIY
X 200 210 220 230 240 250 260

300 310 320 330 340 350 360
LNSSLYRGTKFTIKKYASGNKDNIVRNDRVYINVVKNKEYRLATNASOAGVEKILSALEIPDVGNLSQV
LNSSLYRGTKFTIKKYASGNKDNIVRNDRVYINVVKNKEYRLATNASOAGVEKILSALEIPDVGNLSQV
X 270 280 290 300 310 320 330 340

370 380 390 400 410 420 430
VMSKNDQGITNKKCMNLDQNGNDIGFPHQFNNAKLVASNNYRQIERSRILGCSWEFIPVDDGNGE
VMSKNDQGITNKKCMNLDQNGNDIGFPHQFNNAKLVASNNYRQIERSRILGCSWEFIPVDDGNGE
X 350 360 370 380 390 400 410

X
RPL
RPL
RPL
X

2. US-09-910-186A-2 (1-437)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 193
Residue Identity = 38%
Gaps = 17
Optimized Score = 273
Matches = 169
Conservative Substitutions = 26
Significance = -0.52

X 10 20 30 40 50 60 70
MRLSTFYIKNIINTSILNRYESNHLIDLSRYASKINIGSKYVNFDPIDKNQIQLFNLESSKIEVILANA
FNKYNSEILNHLNRYKDNLDLSGKAVYDGVLELN--DKNQFKLTSSANSKIRVTQNN
X 10 20 30 40 50 60

Copied from 10910186 on 05-05-2004

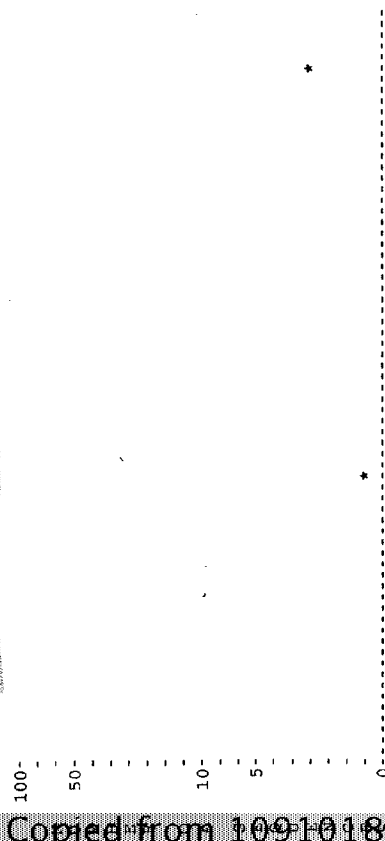
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-3.res made by bobryen on Thu 7 Nov 102 14:40:15-PST.

Query sequence being compared: US-09-910-186A-3 (1-1323)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-3 (1-1323) with:
File: US08123975A.seq



PARAMETERS

Similarity matrix: Unitary
Mismatch penalty: 1
Gap size penalty: 5.00
Gap size penalty: 0.33
Cutoff score: 1
Randomization group: 0

SEARCH STATISTICS

Mean: 1048
Median: 539
Standard Deviation: 442.25
Total Elapsed: 00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sign. Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	1304	1305	0.58
2. US-08-123-975A-1	Sequence 1, Application U	1338	1304	1305	0.58
3. US-08-123-975A-6	Sequence 6, Application U	1351	538	704	-1.15
1. US-09-910-186A-3 (1-1323)	US-08-123-975A-4 Sequence 4, Application US/08123975A				
Initial Score = 1304	Optimized Score = 1305	Significance = 0.58			
Residue Identity = 98%	Matches = 1309	Mismatches = 14			
Gaps = 5	Conservative Substitutions				
X	10 20 30 40 50 60				
GAATTCGAAACGATGCTACCTTCACTGATATCAATCAAGACATCATCAATACCTCCATCTGA					
CTCGAGCCGATGGCTGCTGCTGCTACCTTCACTGATATCAATCAAGACATCATCAATACCTCCATCTGA	10 20 30 40 50 60 70				
70 80 90 100 110 120 130					
ACCTGGCTAGCAATCCCAATCACCTGATCGACCTGCTCGCTAGCTTCCAAATCAACATCGTTCTAAAG					
ACCTGGCTAGCAATCCCAATCACCTGATCGACCTGCTCGCTAGCTTCCAAATCAACATCGTTCTAAAG	80 90 100 110 120 130 140				
140 150 160 170 180 190 200					
TTAATCTCGATCCGATCGCAAGATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAATCGAAGTTATCC					
TTAATCTCGATCCGATCGCAAGATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAATCGAAGTTATCC	150 160 170 180 190 200 210				
210 220 230 240 250 260 270 280					
TGAAGAACTGATCTGATACATCTATGATCGAAATCTTCCACCTCTCTGATCGATCCGGAAT					
TGAAGAACTGATCTGATACATCTATGATCGAAATCTTCCACCTCTCTGATCGATCCGGAAT	220 230 240 250 260 270 280				
290 300 310 320 330 340 350					
ACTTCACTCCATCTCTGACATGATACACATCACTCACTGATCGAATCAATCTGTTGGAAG					
ACTTCACTCCATCTCTGACATGATACACATCACTCACTGATCGAATCAATCTGTTGGAAG	290 300 310 320 330 340 350 360				
TATCTCTGAACTAGCTGAATCATCTGACTCTGACGACACATCAAGAAATCAACAGCGTTGTTATCA					
TATCTCTGAACTAGCTGAATCATCTGACTCTGACGACACATCAAGAAATCAACAGCGTTGTTATCA	360 370 380 390 400 410 420				
430 440 450 460 470 480 490					
ATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGATCTTCTGTTACCATCCCAATCGTC					
ATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGATCTTCTGTTACCATCCCAATCGTC	440 450 460 470 480 490 500				
500 510 520 530 540 550 560					
TGAATACTCCAAATCTACATCAACGCGCTCTGATCGACGAAACCGATCTCCAAATCTGGGTAACATCC					
TGAATACTCCAAATCTACATCAACGCGCTCTGATCGACGAAACCGATCTCCAAATCTGGGTAACATCC	510 520 530 540 550 560 570				
570 580 590 600 610 620 630 640					
ACGCTTCTAATACATCATGTTCAACGCGCTGATCGACGAAATCAACGCTGATCTGGATCAATACT					
ACGCTTCTAATACATCATGTTCAACGCGCTGATCGACGAAATCAACGCTGATCTGGATCAATACT	580 590 600 610 620 630 640				
650 660 670 680 690 700 710					
TCATCTGTCGACAAAGAACTGACGAAAGAAATCAAGAACTGATCGACGAAATCTGATCTGTTATCTGTA					

X 10 20 30 40 50 60
 GAATTCGAACGATGCTCTTCCTTCAGTCATCATCAAGACATCATCATCATCTCCGACCCGCGA
 70 80 90 100 110 120 130
 CTTCGAGCAGCTGGCTGCTCTCTCTTCCTTCCTTCAGTCATCATCAAGACATCATCATCATCTCCGACCCGCGA
 140 150 160 170 180 190 200
 CCTCTCGCTACGATTCATCAATCACTCATGTCAGCTCTCGCTACGCTTCCTTCAGTCATCATCATCTCCGACCCGCGA

[illegible]

[illegible][illegible][illegible]

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TATCGTATTCGARGAATACRAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAACC
1200      1210      1220      1230      1240      1250      1260
1250      1260      1270      1280      1290      1300      1310
TTCCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTTCATCCCGGTTGATGACGGTTGGGTGAACGTCCGCTGTA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
GTACAACCTGAACCTGGGTTGCAATTGGCAGTTTCATCCCGAAGAGAGGTTGGACCCGAATAGTAACCTCT
1270      1280      1290      1300      1310      1320      1330

1320 X
AGAAATTC
| | | |
AGAGTCGAGGCGCTGCAG
1340      1350

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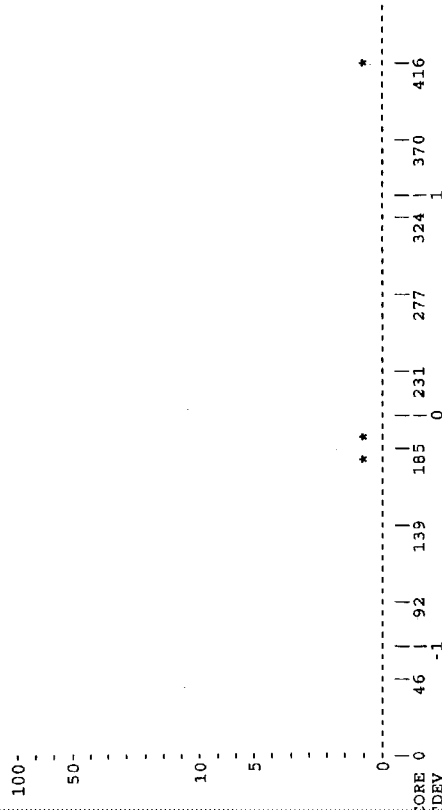

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-4.res made by bobryen on Thu 7 Nov 102 14:32:06-PST.

Query sequence being compared: US-09-910-186A-4 (1-434)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-4 (1-434) with:
File: US08123975A.pep



PARAMETERS

Similarity matrix PAM-150
Threshold level of sim. 16
Mismatch penalty 1
Joining penalty 20
Gap size penalty 5.00
Gap size cutoff score 0.05
Randomization group 0

SEARCH STATISTICS

Scores: Mean 263 Median 181 Standard Deviation 132.66
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Frame
*** 1 standard deviation above mean ***					
1. US-08-123-975A-3	Sequence 3, Application U	415	416	1.15	0
*** 0 standard deviation from mean ***					
2. US-08-123-975A-5	Sequence 5, Application U	439	193	273	-0.53
3. US-08-123-975A-2	Sequence 2, Application U	850	180	275	-0.63

1. US-09-910-186A-4 (1-434)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score = 416 Optimized Score = 416 Significance = 1.15
Residue Identity = 100% Matches = 415 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

MSTFTYIKNIINTSILNRYESNHLIDLSRYASKINIGSKVNFDPIDKNOIQLFNLESSKIEVILKNAIVY
|||||
RYESNHLIDLSRYASKINIGSKVNFDPIDKNOIQLFNLESSKIEVILKNAIVY
X
10 20 30 40 50 60 70

NSMYENFSTFWIRPKYFNSTLNNEYTIINCMEHNSGKWSLYNGELIWTLODTEIKORVVKYSOMIN
|||||
NSMYENFSTFWIRPKYFNSTLNNEYTIINCMEHNSGKWSLYNGELIWTLODTEIKORVVKYSOMIN
60 70 80 90 100 110 120 130 140

ISDYINRWIFVTITNNRLNNSKIYINGRLIDOKPISNLGNHASNIMFKDGCGRDHRVWIKYFNLFDE
|||||
ISDYINRWIFVTITNNRLNNSKIYINGRLIDOKPISNLGNHASNIMFKDGCGRDHRVWIKYFNLFDE
130 140 150 160 170 180 190 200 210

LAKEKEIKDYDQNSGILKDFWGYLOYDKPYMLNLYDPNKYVDVNVGIRGYMYLKGPRGSMVTNIYL
|||||
LAKEKEIKDYDQNSGILKDFWGYLOYDKPYMLNLYDPNKYVDVNVGIRGYMYLKGPRGSMVTNIYL
200 210 220 230 240 250 260 270 280

NSSLYRGTRFIIKKYASGNKDNIVRNDRVYINNVVKNKEVRLATNASQAGVEKILSALEIPDVGNLSQVYV
|||||
NSSLYRGTRFIIKKYASGNKDNIVRNDRVYINNVVKNKEVRLATNASQAGVEKILSALEIPDVGNLSQVYV
270 280 290 300 310 320 330 340 350

MKSKNDQGITNKCKMNLQDNGNDIGFHFHOFNIAKLVASNMYNRQIERSRSLGCSWFEIPVDDGWER
|||||
MKSKNDQGITNKCKMNLQDNGNDIGFHFHOFNIAKLVASNMYNRQIERSRSLGCSWFEIPVDDGWER
350 360 370 380 390 400 410 420 430

X
PL
||
PL
X

2. US-09-910-186A-4 (1-434)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 193 Optimized Score = 273 Significance = -0.53
Residue Identity = 38% Matches = 169 Mismatches = 230
Gaps = 17 Conservative Substitutions = 26

X
10 20 30 40 50 60 70
MSTFTYIKNIINTSILNRYESNHLIDLSRYASKINIGSKVNFDPIDKNOIQLFNLESSKIEVILKNAIVY
|||||
FKNYSEILNLIILNRYKDNLDLSDGKARVEYDGVLEN--DKNQFKLTSSANSKIRVTQNNILF
X
10 20 30 40 50 60


```

80      90      100      110      120      130      140
NSMYEFSFWIRIPKYPNSIS---LNNEYTIINCMMNSGWKSVLNGYELIWTLDQTQEI KORVVFYSQ
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
NSYLFDSVSEFWIRIPKYPNDGQIYHNEYTIINCMMNSGWKSVLNGYELIWTLDIDINGKTSVFEYNI
70      80      90      100      110      120      130
150      160      170      180      190      200      210
MINISYINRWIVTITNNLNNSKIYINGRLIDOKPISNLGNHASNNIMFKLDGCRDTHRYIWKYFNLF
||:|||||:|||||:|||||:|||||:|||||:|||||:
REDISYINWVFTITNN-LNNAKIYINGKLESNTDKIDREVIANGELIIFPKLDGDDIDRTQFIWMIYFIF
140      150      160      170      180      190      200      210
DKELNEKEIKLDYDQNSGILKDWGDLQYDKPKYMLNLYDPNKYVDVNNVGRGYMYLKGPRGVMVTN
220      230      240      250      260      270      280
NTELSSNTEERYKIQSYSEYKLDWGNELMKNKEYYMFNAGNKNKYIKLKKDPSVGEILTRSKYNNNSKYI
220      230      240      250      260      270      280
290      300      310      320      330      340      350
IYLNSSLYRGTKFIIKKYASGKNKIVNRNDRVYINVVYKKNKEYLATNASQAGVERKILSALEIPDYGNLSQ
||:|||||:|||||:|||||:|||||:|||||:
NYRDLVIGKEFIIRRKSNQSINDDIVRKEDYIYLDFFNLQEWVRVYTYKYFKKEEKLFLAPISDSDEFYN
290      300      310      320      330      340      350
360      370      380      390      400      410      420
VYVWKSNDQGI-TNCKKNLQNNNDIGFHFQFNNAKLVA-----SNWYNRQIERS--SRTLGC
||:|||||:|||||:|||||:|||||:|||||:
TIQIKVEQPTYSCQLFKDEESTDEIGLICIHRYFESGTVFEEYKDYFCISKWYLKEVKRKPYNLKGCC
360      370      380      390      400      410      420
420      430
SWEFIPVDDGWERPL
||:|||||:
NWQFIPKDEGWE
430      X

```

US-09-910-186A-4 (1-434)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score = 180 Optimized Score = 275 Significance = -0.63
Residue Identity = 37% Matches = 169 Mismatches = 233
Gaps = 17 Conservative Substitutions = 26

```

X      10      20      30      40      50
MSTFTYIKNIINTSILNRYESNHLIDLSRYASKINIGSKVNFDPIDKNOI
KYLKTIMPDLSTYNTDILIEFMFNKYNSEILNLIILNRYKDNLDLSGYGAKVEYDGVELN--DKNQF
390      400      410      420      430      440      450
60      70      80      90      100      110      120
QLPNLESSKTEVLKNAIVYNSMYENFSFWIRIPKYPNSIS---LNNEYTIINCMMNSGWKSVLNGYELI
||:|||||:|||||:|||||:|||||:|||||:
KLTSSANSKIRVTQONQIIFNSVFLDVSFWIRIPKYPKNDGQIYHNEYTIINCMMNSGWKSVLNGYELI
460      470      480      490      500      510      520      530
130      140      150      160      170      180      190
IWTLDQTQEI KORVVFYSQMINISYINRWIVTITNNLNNSKIYINGRLIDOKPISNLGNHASNNIMF
||:|||||:|||||:|||||:|||||:|||||:
IWTLDINGKTSVFEYINREDISEYINRWVFTITNN-LNNAKIYINGKLESNTDKIDREVIANGELIF
540      550      560      570      580      590      600
200      210      220      230      240      250      260
KLOGCRDTHRYIWKYFNLFKELNEKEIKLDYDQNSGILKDWGDLQYDKPKYMLNLYDPNKYVDVNN
||:|||||:|||||:|||||:|||||:|||||:
KLDGDDIDRTQFIWMIYFIFNTELSQNSIEERYKIQSYSEYKLDWGNELMKNKEYYMFNAGNKNKYIKLKK
610      620      630      640      650      660      670
270      280      290      300      310      320      330
VGLRGWYILKGPAGSVMTTINLNSLYRGTKFIIKKYASGKNKIVNRNDRVYINVVYKKNKEYLATNASQ
||:|||||:|||||:|||||:|||||:|||||:
DSPVGEILTRSKYNNNSKYINRDLVIGKEFIIRRKSNQSINDDIVRKEDYIYLDFFNLQEWVRVYTYKYF

```

Sequence Name	Description	Length	Score	Init. Opt.	Sig. Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	1302	1307	0.58
2. US-08-123-975A-1	Sequence 1, Application U	1338	1302	1307	0.58
3. US-08-123-975A-6	Sequence 6, Application U	1351	538	704	-1.15
1. US-09-910-186A-5 (1-1326)	Sequence 4, Application US/08123975A				
Initial Score	= 1302	Optimized Score	= 1307	Significance	= 0.58
Residue Identity	= 98	Matches	= 1311	Mismatches	= 15
Gaps	= 5	Conservative Substitutions	=		= 0

Results of the initial comparison of US-09-910-186A-5 (1-1326) with:
File: US08123975A.seq

[illegible]

TATCTCTGAACCTACGGTGAATCATCTCGGACTCTCGAGGCACTCAGGAATCAAACAGCGGTCTGTATTCA
360 370 380 390 400 410 420

TATCTCTGAACCTACGGTGAATCATCTCGGACTCTCGAGGCACTCAGGAATCAAACAGCGGTCTGTATTCA
370 380 390 400 410 420

ACHTCAACTCCGATCTCTTGACAACTAATAACACCACATCATCAACTGCATGGAACAACATCTCGTTGGAAA
290 300 310 320 330 340 350 360

430 440 450 460 470 480 490
 AATACCTCAGATGATCAACATCTCTGACTATCATCAATCGCTGGATCTTCGTACCATCCACCAATGCTC
 AATACCTCAGATGATCAACATCTCTGACTATCATCAATCGCTGGATCTTCGTACCATCCACCAATGCTC
 AATACCTCAGATGATCAACATCTCTGACTATCATCAATCGCTGGATCTTCGTACCATCCACCAATGCTC
 440 450 460 470 480 490 500
 500
 TGAATACTCCAAATATACATCAACGCGCGTGTGATCACCAGAAACCGATCTCCATCTGGGTAAACATCC
 TGAATACTCCAAATATACATCAACGCGCGTGTGATCACCAGAAACCGATCTCCATCTGGGTAAACATCC
 510 520 530 540 550 560 570
 TGAATACTCCAAATATACATCAACGCGCGTGTGATCACCAGAAACCGATCTCCATCTGGGTAAACATCC
 520 530 540 550 560 570

ACGGTTCTTAATACACATCATGTTTCAACGTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAACTACT
580 590 600 610 620 630 640

TCAATCTGTTTCGACAAAGAAGCTGACGAAAAAGAGAAATCAAAGACCTGTACGACCAACCCTCCAAATTCCTGGTA

Copied from 10910186 on 05-05-2004

[illegible]

790 800 810 820 830 840 850
ACAAATACGTTGACGCTCAACAACTTAGTATCCGCGTTACCTGTAAGGTCGCGTGGTTCGTGTA
ACAAATACGTTGACGCTCAACAACTTAGTATCCGCGTTACCTGTAAGGTCGCGTGGTTCGTGTA

[illegible]

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0 | 0 IntelliGenetics
> 0 <

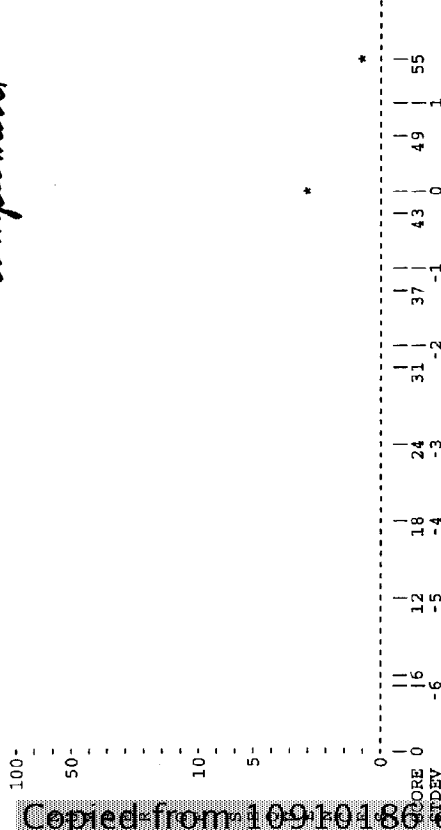
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-5-inv.res made by bobryen on Thu 7 Nov 102 14:41:54-PST.

Query sequence being compared: US-09-910-186A-5' (1-1326)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-5' (1-1326) with:
File: US08123975A.seq

complement



PARAMETERS
Unitary K-tuple 4
Mismatch penalty 30
Gap size penalty 5.00
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS
Mean Median Standard Deviation
47 45 6.35
CPU 00:00:00.00
Total Elapsed
00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.
1. US-08-123-975A-6	Sequence 6, Application U 1351	55	430	1.26
2. US-08-123-975A-4	Sequence 4, Application U 1338	44	478	-0.47
3. US-08-123-975A-1	Sequence 1, Application U 1338	44	478	-0.47

1. US-09-910-186A-5' (1-1326)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 55
Optimized Score = 430
Significance = 1.26
Residue Identity = 40%
Matches = 519
Mismatch = 665
Gaps = 89
Conservative Substitutions = 0

80 90 100 110 120 130 140 150
CGTTTCGATCTGACGATTGTCACAGTTGGAAGCAACAGTTTACGATATTTGTTGAAGTGGTGAACCGGATG
ATGGCTTTCAACAAATACAAATTCGGAATTCCTGCAACATATCATCTGGAAC
X
160 170 180 190 200 210 220
AAACCGATATCGTTTACCATTTGTTCTGCTGAGATTTTCATTTGATTTAGTGATACCTGGTCTGTTCTTGG
TCGTTTACAAGACACAAATCTGATCGATCTGCTGTTAGCGTGAAGTTGAAGTATACACCGGTGTTG
60 70 80 90 100 110 120
230 240 250 260 270 280 290
GATTTTCAATACAACTACCTGAGACAGATTTACACGTCGCGGATTTCCAGACAGACAGATCTTTTCTAC
AACTGATGACAAAGAACCGAG-TTCAAACTGACCTCTCCGCTAACCTC-----TAAGATCCGTTTAC-
130 140 150 160 170 180
300 310 320 330 340 350 360
CCAGCTGAGAAAGCATTTGTTAGCAGACGATTTCTTTGTTTAACTACACATGATGATACACGATCA
TCAGAAATCAGAA-CATCATCTTCACTCCGATTTCTCTG-----ACTTCTGTTCTCTCTGATGC
190 200 210 220 230 240
370 380 390 400 410 420 430
TTGTTGCAACGATATTTCTCTGTTA-CCAGACGCGTATTTCTGATGATGATGATTTGGTACACCGGTAC
GTATCCGAAATACAAAGACAGCGGTATCCAGATTTACATCCCAATGATACACCATCATCATCATGATGA
250 260 270 280 290 300 310
440 450 460 470 480 490 500
GGAAGATTCAGGT-----AGATGTTGTT-AGTCATACAGACACGCGGACCTTTTACGATACATGATACCG
AGATTAATCTGTTGGAAGATCTCCATCCGCGGTAAACCGTATCATCTGGAC---TCTGATGATATCAACG
320 330 340 350 360 370 380
510 520 530 540 550 560 570
CGGATACCTACATTTGTTGACGTCAACGATTTTGTTCGGATCGTACAGATTCAGCATGATAGTACGGTTTGTG
GTACACCAAAATCTGTTCTTCCA-ATACAAATCCGTTGAAGNCA---TCTGATACATCAATCAACCGTTG
390 400 410 420 430 440 450
580 590 600 610 620 630 640
TACTGAGGTAGTACCCACGAGATCTTTTCCAGATACCAAGTTGGACTGTTGTTGTTGTTGTTGTTGTTGTT
TTCCTC--GTTACCATCACCAATTAACCTGACATGCTAAATCTCATCAACGTTAAACCTGGAATCTAATA
460 470 480 490 500 510 520
650 660 670 680 690 700 710
TCTTTTTCGTTTCAGTTC-----TTTTCGAACAGATTTGAA---GTATTTTATCCAGATGATACCGTTGATG
CCGACATCAAGACATCGTGAAGTTATCGTTACCGGTGAATCATCTTCAAACTGACGCGTACATCATGATC
530 540 550 560 570 580 590
720 730 740 750 760 770
TCACGACAAACCGTCCAGTTTGAACATGATGTTATAGAACGGTGAATTTACCCAG-----ATTGGAGATC

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600 610 620 630 640 650 660 670
GTACCCAGTTTCATCTGGATGAATACCTTCTCCATCTTCAACACCGAAGTCTCTCAGTCCAAATATCGAAGAAC
|||||
780 790 800 810 820 830 840
GGTTCTGGTTCGATCAGACGGCGGTTGATGT---AGATTTGGAGTTATTACAGAGATGTTGGTGAGGTA
|||||
850 860 870 880 890 900 910
ACGAGATCCAGCGATTTGATGTAGTACAGATGTTGATCTATCTGAGAGATTTGATACACACCGCTGTTTG
|||||
920 930 940 950 960 970 980
ATTTCCTGAGTGTCTCCAGATCCAGATGATTTACCGGTAGTTCA-----GAGATACTTTCCACACAGAA
|||||
990 1000 1010 1020 1030 1040 1050
TGTTTTTCCATGC-----AGTTGATGATGGTGTATTCATTTCTCAGAGAGATGGAGTTGAAGTATTTTCGG
|||||
1060 1070 1080 1090 1100 1110
GATACGGA-----TCCAGAGAGAGGTGGAGAGTTTCCTGATACAGATGTTGATAGATGAGATTTCTTCAGG
|||||
1120 1130 1140 1150 1160 1170 1180
ATAACTTCGATTTTGGAGATTCAGATTAAGACAGTGGATCTGATCTTCTGATGATCGATCGAATTAAC-
|||||
1190 1200 1210 1220 1230 1240 1250
-ITTAGACCGA--TGTTGATTTGGAGAGGTGCGAGACAGTGCATCAGGTGATGTTGATTCGTAGCCGAG
|||||
1260 1270 1280 1290 1300 1310 1320
GTTACGATGGAGTATGATGATGTTCTTGATGATTTAGTGAAGTAGAGCCATCGTTTTCGATTC
|||||
1330 1340 1350 1360 1370 1380 1390
ATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAAATACAAAGACTACTTCTGCATCTCCAA
1170 1180 1190 1200 1210 1220 1230
TGGTACCTGAAGGAAGT
1240 1250

2. US-09-910-186A-5' (1-1326)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 44 Optimized Score = 478 Significance = -0.47
Residue Identity = 43% Matches = 582 Mismatches = 681
Gaps = 78 Conservative Substitutions = 0

10 20 30 40 50 60 70
GAATTTTACAGCGGACGCTTCAACCCACCGTATCAACCGGATGAATCCCAAGAGCAACCGAGTGGC
|||||
80 90 100 110 120 130 140
ACAGAGAGGTTCGATCTGACGATTTGATACAGTGGAGAGCAACAGTTTACGATGATTTGTTGAACTGGTGAA
|||||
ATCAATACCTCCATCTGTA-----ACCTGCGCTAGCAATCAATCACTGATCGACCTGTTCTGCT--AC
|||||
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150 160 170 180 190 200 210
ACCGATGAACACCATATCGTTTACCATTGTTTGCTCCAGATTCATTTTGCATTTGTTAGTGATACCTTGGTC
|||||
120 130 140 150 160 170 180
GCTTCCAAATCAACATCGGTTCTAAAGTTACTT---CGATCCGATCGAAGAAATCAGATCCCA--GCTGTTC
|||||
220 230 240 250 260 270 280
GTTCTTGGATTTTCATTAACAATACCTTGAGACAGATTAACAAGTCCCGGATTTCCAGACGACAGATGATCTT
|||||
290 300 310 320 330 340 350
AATCTGGAATCTTCCAAATTCGAAGTTATCC---TGAAGATGCTATCTGATACACTCTATGTCAGAAAC
|||||
360 370 380 390 400 410 420
TTCTACACCGAGCTTGAAGATGTTGTTAGCAGACGATTTCTTCTTAACACTACAACATGATGATATAC
|||||
430 440 450 460 470 480 490
CCACGGTACAGGGAAGAGTTCAGTATGTTGTTGTTTACCAGACGC--GTATTTCTTGTATGATGAATTTGGTA
|||||
500 510 520 530 540 550 560
ATGTATCCGGGGATACCTATGTTTACCTCAACGTATTTGTTGCGA--TCGTACAGATTCAGATGATAGT
|||||
570 580 590 600 610 620 630
ACGGTTTG--TCGTTACTCAGGTAGTCAAC---CCAGAAGTCTTTCAGGATACAGAAATGGACTGGTTGCG
|||||
640 650 660 670 680 690 700
TACAGGTCTTTGATTTCTTTTCTGTTCTCAGTTCCTTTCGAAACAGATTTGAAGTATTTGATCCAGATGTCAGCG
|||||
710 720 730 740 750 760 770
TGAGTGTACAGACACCGCTCCAGTTTGAACATGATGTTATAGAAGCGTGGATGTTTACCCAGATTTGGAGATC
|||||
780 790 800 810 820 830 840 850
AAG-----ATCCACCGATTTGATGTTAGTACAGAGATGTTGATCATCTCAGAGATTTTGAATACACACGCTGTT
|||||
860 870 880 890 900 910
ATGAGTATTCGCGGTTTACATGTA---CCTGAAGGTCCGCGTGGTTCTGT--TATGACTACCAACATCTACC
820 830 840 850 860 870 880
920 930 940 950 960 970 980
TGATTTCTGAGTCTCTCGAGAGTCCAGATGATTTCCCGTAGTTTCAGAGTACTTTTCCACACCAATTTGT
|||||
990 1000 1010 1020 1030 1040 1050
TGAACTTCTCCCTGATCCG--TGGTACCAATTCATCATCAAGAAATACCGGCTCTGTATACAGGACAAATATC
890 900 910 920 930 940 950
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[illegible]


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||||| 930 940 950 960 970 980 990
AGAAATACCGGCTCTGGTAAACAGGACAAATATGTTGCGAACAATGATCGGTATATACATCAATGTTGTAGTTA
980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130
TGAATCAGGAATGGGTGTATACACCTACAGTACTTC-AAGAAGAGAGAGAAAGCTTTCTCGCTCGG
||||| 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130
AGACAAAGAAATACGGTCT- - - - -GCTACCAATGCTTCTCAGGCTGGTGTGAGAAAGATCTGTCTGCTGTG
1050 1060 1070 1080 1090 1100 1110 1120 1130
---ATCTCTGATTCGACGAACTCTACACACCATCCAGATCAAGAAATACGACAGCAGCGACCTACCTCT
GAAATCCCGAGGCTGGTAAATCTCTCAGGTAGTGTGAATGAATCCAGAAAGACAGCGGTA---TCACT
1070 1080 1090 1100 1110 1120 1130
1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260
TGCACGCTCTGTTCAAGAAAGATGAAGAATCTACTGAGAAATCGGTCTGATCGGTATCCACCGTTTCTAC
||||| 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260
AACAAATGCAAAATGAATCTGCAGGACACAAATGTAACGATATCGGTTTCATCGGTTCCACCGATTCAAC
1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260
1190 1200 1210 1220 1230 1240 1250 1260
GAATCGGTATGTAATCGAAGAAATACAAAGACTACTTCTGCATCTCCAAATGCTACTGAAAGAACTAAA
||||| 1210 1220 1230 1240 1250 1260
AA-----TATCG-----CTAAACTGGTTGCT-----TCCAAGTGGTAC-----AATCGTCAAG
1210 1220 1230 1240 1250 1260
1270 1280 1290 1300 1310 1320 1330 1340
CGAAACCGGTACAACTGAAATGGGTGCAATGGAGTTCATCCGAAAGACGAGGTGGACCGAAATAG
||||| 1270 1280 1290 1300 1310 1320 1330 1340
ATCGAAGTTCCTCTCCGACTCTGGCTCTCTGGAGTTCATCCCGGTTGATCGGTTGGGGTGAAGCT
1250 1260 1270 1280 1290 1300 1310 1320 1330 1340
TAAGAAATTC
CGCGTGTAAACCGGGAAAGCTT
1320 X 1330
US-09-910-186a-7 (1-1341)
US-08-123-975A-1 Sequence 1, Application US/08123975A
Initial Score = 533 Optimized Score = 699 Significance = -0.58
Residue Identity = 55% Matches = 754 Mismatches = 535
Gaps = 71 Conservative Substitutions = 0
X 10 20 30 40 50
GAATTCAGATGCGCCAAACAATACAAATTCGGAATCTCTGACAAATATCATCTTGA
CTCGAGCGAATGGCTGCTGCTGCTACCTTCACTGAATACATCAAGAAACATCATCACTCCATCCCTGA
10 20 30 40 50 60 70
60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330
ACCTGGTTTACAAAGACAAATCTGATGATCTCTGCTGGTTACGCTCTAAAGTGAAGT--ATAGACGG
||||| 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330
T-----GTGAACTGAATGACAAAGACCACTTCAAACTGACCTCTTCCGCTAACTCTAAAGTCCGCTGATCTC
TTAACTTCGATCGATCGACAGATCAGATCCAGCTGTTCAATCTGGAATCTCCAAATCCGAAGTTATCC
150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330
200 210 220 230 240 250 260 270 280 290 300 310 320 330
AGAATCAGAACATCATCTTCAACTCGGTATTCCTGAGCTCTCTGTTTCTTCTGGATTCGATCCCGGAAT
||||| 210 220 230 240 250 260 270 280 290 300 310 320 330
TGAAGAAATGATATGATACAACTCTATGAGAAATCTTCCACCTCTCTGATCGGTTGATCCCGGAAT
220 230 240 250 260 270 280 290 300 310 320 330

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ACAAAGACAGCGGTATCCAGAAATATACATCCACAATGAATACACATCATCACTGATGAAGAAATACACTCTG
||||| 310 320 330 340 350
ATTCTCAACTCC-----ATCTCTGTGAACAATGAATACACCATCATCACTGCAAGAAACAAATCTGTG
290 300 310 320 330 340 350
340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490
GTGGAAGATCTCCCAATCCCGGTAACTCATCTGACCTCTGATCATCAACGGTAAAGACCAATCTG
||||| 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490
GTGGAAGATCTCTCTGAACCTACCGGTGAATCATCTGGACTCTGCAGGACACTCAGGAATCAACAGCTGG
360 370 380 390 400 410 420 430 440 450 460 470 480 490
410 420 430 440 450 460 470 480 490
TATTTCTCGAATACCAACCTCCGTAAGACATCTCTGAATACATCAATCGCTGTTCTTCTGTTACCATCACA
||||| 410 420 430 440 450 460 470 480 490
TTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGTTCTGTTACCATCACA
430 440 450 460 470 480 490
430 440 450 460 470 480 490
ATATA-----CCTGAACAATGTAATAATCTACATCAACGGTAACTGTAATCTAATACCGACATCAAGACATCC
490 500 510 520 530 540 550
ACAAATCGTCTGATTAACCTCAAAATCTACATCAAGCGCTCTGATCGACCAAGAAACGATCTCCAACTCTGG
500 510 520 530 540 550 560
560 570 580 590 600 610 620
GTGAAGTTATCTGCTAACGCTGAATATCTTCAACTGAGCGGTGACATCGATCGTACCGAGTTCTATCTGGA
||||| 560 570 580 590 600 610 620
GTAACATCCACGCTTCTTAATAACATCATGTTCAACTGAGCGTGTGCTGACACTCACCGCTACATCTGGA
570 580 590 600 610 620 630
630 640 650 660 670 680 690 700 710
TGAATATCTTCTCCATCTTCAACACCGAACTGCTCAGTCCAAATATCGAAGACGGTACAGATCCAGTCTT
||||| 630 640 650 660 670 680 690 700 710
TCAAAATCTCTAACTGTTGCAACAAGAACTGAACGAAAGAAATCAAGAACCTGTACGACAAACCACTGCA
640 650 660 670 680 690 700 710
700 710 720 730 740 750 760 770 780
ACTCCGAATACCTGAAAGACTTCTGGGTAACTCCCTGATGTACAAACAAAGAAATCTATATGTTCAATGCTG
||||| 700 710 720 730 740 750 760 770 780
ATTCTGTTATCTGAAAGACTTCTGGGTGATCTACCTGCTACGACAAACCGTACATCTGATGTAATCTGT
720 730 740 750 760 770 780
770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920
GTAACAGAACTCTTACATCAACTGAAGAAAGACTCTCCGGTTGGTGAAT---CCTGACTGCTTCCAAAT
||||| 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920
ACGATCCGAAACAAATGATGCTGACGTCACCAATGTAGGTATCCGGGTTACATGACCTGAAAGTCCGCGTG
790 800 810 820 830 840 850 860 870 880 890 900 910 920
840 850 860 870 880 890 900
ACAAACAGAACTCTAAATACATCAAC---TACCGGACCTGTACATCGGTGAAAGTTCATCATCCGTCGCA
||||| 840 850 860 870 880 890 900 910 920
GTTCTGTTATGACTACCAACATCTTACCTGAACTTCTCCCTGTACCGGTGGTACCAATTCATCAT-----CA
860 870 880 890 900 910 920
910 920 930 940 950 960 970 980 990
AATCTAACCTCTCAGTCCATCAATGATGATCGTACGTAAAGAAAGACTACATCTACCTGGACTTCTTCAACC
||||| 910 920 930 940 950 960 970 980 990
AGAAATACCGGCTCTGTTACAGGACATATGTTCTCGCAACAAATGATCGTGTATACATCAATGTTGTAGTTA
930 940 950 960 970 980 990
980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130
TGAATCAGGAATGGGTGTATACACCTTACAGTACTTC-AAGAAGAGAGAGAAAGCTTTCTCGCTCGG
||||| 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130
AGAAACAAAGAAATACGCTCT- - - - -GGCTACCAATGCTTCTCAGGCTGGTGTAGAAAGATCTGTCTGCTCTG
1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130
1050 1060 1070 1080 1090 1100 1110 1120 1130
---ATCTGATTCGAGAACTCTACACACCATCCAGATCAAGAAATACGACAGCAGCGCTACCTCT
||||| 1050 1060 1070 1080 1090 1100 1110 1120 1130
GAAATCCCGAGGCTGGTAAATCTCTCAGGTAGTGTGAATGAATCCAGAAAGACAGCGGTA---TCACT
1070 1080 1090 1100 1110 1120 1130
1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260
TGCCACCTCTGTTTCAAGAAAGATGAAGAATCTTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTAC
||||| 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260

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[illegible]

GAATTCCTACTATTCGGTCCAACTTCGCTCTTTCGGGATGAACCTGCCAATGAACCCAGCTTTCACAGTTGTTAT
 CFCGAGCCATCGCTCGCTCTGCTGTCCTACCTTCACTGAATACATCAAGAACATCATCATCAATA
 X 10 20 30 40 50
 80 90 100 110 120 130 140
 CGGTTTCGGTTTAACTTCCTTCAGGTACCATTTGGAGATGCAGAAAGTASTCTTTGTATTCTTGGATA-CGA
 CCTCCATCCTCAACTCGCTGCTACGAATCCAAT-CACCTGATCGACCTGCTTCGCTACGGTCTCCAAAATCAA
 70 80 90 100 110 120 130
 150 160 170 180 190 200 210
 TACCAGATTCGTAGAAAAGCGTGGAT---ACCGATCAG-ACCGATTTCCTCAGTAGATCTTCATCTTCCTTTG
 CATCGTTCTAAAGTTAACTTCGATCCGATCGACAGAAATCAGATCCACAGCTGTTTCAATCTTGGAACTTCCAA
 140 150 160 170 180 190 200
 AACACAGCTGGCAGAGTAGTAGTCGGCTGTCGTATCTTCTGATCTGGATGGTGTGTAGAGTTCGTCTG
 AATCGAAGTATCTCTGAGAATGC-----TATCTATACAACTCTATGTACGAAACTT---CTCCACCT
 210 220 230 240 250 260 280
 290 300 310 320 330 340 350
 GAATCAGATCGGAGCGCAGAAAGCTTTCTCTCTTCCTGAGTACTTGTAGTGTATACAGCCGAT
 CTTCTCGATCGTATCCCGAATATCTTCAACTCCATCTCTGAA-----CAATGATACAC-CATC
 270 280 290 300 310 320
 360 370 380 390 400 410
 TCTGATTCAGGTTGAAGAAGTCCAGGTAGATAGTCTTCTTACGTACGATGTCAATC-----TGA
 ATCAACTGCATGGAACAAATCTCTGGTTGA--AAGTATCTCTGAACTACGGTGAATCATCTGGACTCTGC
 330 340 350 360 370 380 390
 420 430 440 450 460 470 480
 TGGAC---TGAGAGTTAGATTGGCAGGATGAAGACTTTCAACGATGATCAGGTGCGGTAGTTGATGT
 AGSACACTCAGGAATCAACAGCGGTGTTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCA
 400 410 420 430 440 450 460
 490 500 510 520 530 540 550
 AT--TTAGAGTCTGTTGTTGTTGGAACG--GTCAGGATTTCAACACGGAGAGTCTTTCTTCAGTTG
 ATCGCTGGATCTCTGTTACCATACCAACAAATCGTCTGAAATCTCCAAATCTACATC-AACGGCGTCTG
 470 480 490 500 510 520 530
 560 570 580 590 600 610 620
 ATGTAAGATCTCTGTTACCAGCATGAAATATAGTATCTTGTGTATCATCAGCGAATATCCCGAGAAG
 ATCGCCAGAACCCGATCTCCAATCTGGGTAAACATCCACGCTCTTAATAACATCATGTTCCTCAACTGGACGGT
 540 550 560 570 580 590 600 610
 630 640 650 660 670 680 690
 TCTTTCAGTATTCGGAGTAGACTGGATCTTTGAC-----CGTCTTCGATATTGGATCGAGACAGTTCGGT
 TGTGCTGACACTCGCGGTACATCTGGATCAAAATCTCAATCTCTCCACAAAGAACTGGAACGAAAAAGAA
 620 630 640 650 660 670 680
 700 710 720 730 740 750
 GTTGAAGA-----TGAGAGATATTTC-ATCCAGATGAATCGGTACGATC---GATGTCACCGTCCAGTTT
 ATCAAAGACCTGTACGACCAACCGATCCAAATCTGTTATCTGTAAAGACATCTTGGGTGACTACCTGCGAGTAC
 690 700 710 720 730 740 750
 760 770 780 790 800 810 820
 GACAAACCGTACTACATGCTGAATCTGTACAGATCCGAAACAATACGTTGAGCTCA--ACAATGTAGGTATCC
 760 770 780 790 800 810 820
 830 840 850 860 870 880 890
 GTTGATGTAGATTTAGCATTTCTCAGGTATTT-GTGTATGGTGAACGAAACACCGAGTTCGATGTATTCAC
 GTTGATGTAGATTTAGCATTTCTCAGGTATTT-GTGTATGGTGAACGAAACACCGAGTTCGATGTATTCAC

```
Initial Score      = 43  Optimized Score = 481  Significance = -0.47
Residue Identity  = 42%  Matches      = 577  Mismatches  = 716
Gaps              = 79   Conservative Substitutions = 0
```

10	x	20	30	40	50	60	70
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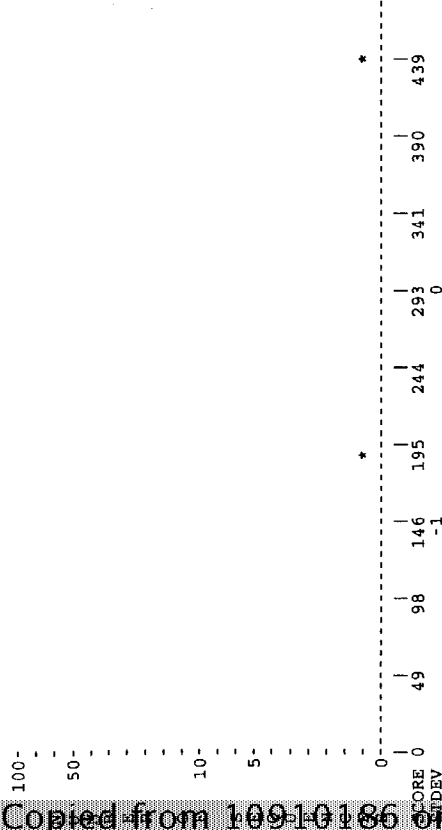
> O <
O/ IO IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-8.res made by bobryen on Thu 7 Nov 102 14:32:54-PST.

Query sequence being compared: US-09-910-186A-8 (1-440)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-8 (1-440) with:
File: US08123975A.pep



PARAMETERS

Similarity matrix PAM-150
Threshold level of sim. 16%
Mismatch penalty 1
Gap penalty 5.00
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 355 Median 190 Standard Deviation 144.05
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Opt.	Score	Sig.	Frame
1. US-08-123-975A-2	Sequence 2, Application U	850	439	439	0.58	0
2. US-08-123-975A-5	Sequence 5, Application U	439	438	438	0.58	0
3. US-08-123-975A-3	Sequence 3, Application U	415	189	259	-1.15	0

1. US-09-910-186A-8 (1-440)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score = 439
Residue Identity = 99%
Gaps = 0
Optimized Score = 439
Matches = 438
Significance = 0.58
Substitutions = 0
Mismatched = 2

X 10 20 30 40 50
MANKYSEILNNILNRYKDNLDLSGYGAKVEYDGVDELNDKNQFKLTS
LKTIMPDLSTYNTDILIEFMENKYNSEILNNILNRYKDNLDLSGYGAKVEYDGVDELNDKNQFKLTS
60 70 80 90 100 110 120
SANSKIRVTQNONIIFNSVFLDFSVFWIRPKYKNDGIONYIHNEYTIINCKNNSGKISIRGNRIIWTIL
SANSKIRVTQNONIIFNSVFLDFSVFWIRPKYKNDGIONYIHNEYTIINCKNNSGKISIRGNRIIWTIL
130 140 150 160 170 180 190
IDINGKTKSVFEYNIREIDSEYINRWFFVTITNNLNNAKIYINGKLESNTDIDKIDREVIANGEIIFKLDGD
IDINGKTKSVFEYNIREIDSEYINRWFFVTITNNLNNAKIYINGKLESNTDIDKIDREVIANGEIIFKLDGD
200 210 220 230 240 250 260
IDRTOFIMWKYFSIFNTLSQSENEERYKIQSYSEYLDKFWGNPLMYNKEYYMFNAGNKNYSIKLAKDSPVG
IDRTOFIMWKYFSIFNTLSQSENEERYKIQSYSEYLDKFWGNPLMYNKEYYMFNAGNKNYSIKLAKDSPVG
270 280 290 300 310 320 330 340
EILTRSKYNQNSKYINVRDLYIGKEFIIRKKSQSINDDIVRKEDYIYLDFFNLNQEWVRVITYKYFKKEEE
EILTRSKYNQNSKYINVRDLYIGKEFIIRKKSQSINDDIVRKEDYIYLDFFNLNQEWVRVITYKYFKKEEE
350 360 370 380 390 400 410
KLFLAPISDSDELNTYNTIQIKEYDEQPTYSQQLLFKDEESTDEIGLIHFRFYESGIVFEEYKDYFCISKWY
KLFLAPISDSDELNTYNTIQIKEYDEQPTYSQQLLFKDEESTDEIGLIHFRFYESGIVFEEYKDYFCISKWY
420 430
LKEVRRKYPYNLKLGCNWFQIFPKDEGWTE
LKEVRRKYPYNLKLGCNWFQIFPKDEGWTE
830 840 850

2. US-09-910-186A-8 (1-440)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 438
Residue Identity = 99%
Gaps = 0
Optimized Score = 438
Matches = 437
Significance = 0.58
Substitutions = 0
Mismatched = 2

X 10 20 30 40 50 60 70
MANKYSEILNNILNRYKDNLDLSGYGAKVEYDGVDELNDKNQFKLTS
LKTIMPDLSTYNTDILIEFMENKYNSEILNNILNRYKDNLDLSGYGAKVEYDGVDELNDKNQFKLTS
60 70 80 90 100 110 120
SANSKIRVTQNONIIFNSVFLDFSVFWIRPKYKNDGIONYIHNEYTIINCKNNSGKISIRGNRIIWTIL
SANSKIRVTQNONIIFNSVFLDFSVFWIRPKYKNDGIONYIHNEYTIINCKNNSGKISIRGNRIIWTIL
130 140 150 160 170 180 190
IDINGKTKSVFEYNIREIDSEYINRWFFVTITNNLNNAKIYINGKLESNTDIDKIDREVIANGEIIFKLDGD
IDINGKTKSVFEYNIREIDSEYINRWFFVTITNNLNNAKIYINGKLESNTDIDKIDREVIANGEIIFKLDGD
200 210 220 230 240 250 260
IDRTOFIMWKYFSIFNTLSQSENEERYKIQSYSEYLDKFWGNPLMYNKEYYMFNAGNKNYSIKLAKDSPVG
IDRTOFIMWKYFSIFNTLSQSENEERYKIQSYSEYLDKFWGNPLMYNKEYYMFNAGNKNYSIKLAKDSPVG
270 280 290 300 310 320 330 340
EILTRSKYNQNSKYINVRDLYIGKEFIIRKKSQSINDDIVRKEDYIYLDFFNLNQEWVRVITYKYFKKEEE
EILTRSKYNQNSKYINVRDLYIGKEFIIRKKSQSINDDIVRKEDYIYLDFFNLNQEWVRVITYKYFKKEEE
350 360 370 380 390 400 410
KLFLAPISDSDELNTYNTIQIKEYDEQPTYSQQLLFKDEESTDEIGLIHFRFYESGIVFEEYKDYFCISKWY
KLFLAPISDSDELNTYNTIQIKEYDEQPTYSQQLLFKDEESTDEIGLIHFRFYESGIVFEEYKDYFCISKWY
420 430
LKEVRRKYPYNLKLGCNWFQIFPKDEGWTE
LKEVRRKYPYNLKLGCNWFQIFPKDEGWTE
830 840 850

```

80 90 100 110 120 130 140
LDFSVFWIRPKYKNDGIONYNHETIINCNNKNSGKISIRGNRIITWLDIDNGKTSVFFEVNIREDI
|||||
LDFSVFWIRPKYKNDGIONYNHETIINCNNKNSGKISIRGNRIITWLDIDNGKTSVFFEVNIREDI
80 90 100 110 120 130 140
150 160 170 180 190 200 210
SEYNIRWFEVITNNLNAKIYINGKLESNTDIKIDREVIANGELIIFKLDGIDRTQFIWMKYFSIFNTELS
|||||
SEYNIRWFEVITNNLNAKIYINGKLESNTDIKIDREVIANGELIIFKLDGIDRTQFIWMKYFSIFNTELS
150 160 170 180 190 200 210
220 230 240 250 260 270 280
QSNIEERYKIQSYSEYKDFWGNPLMYNKYYFNAGKNKSYIKLAKDSPVGEILTRSKYNQNSKYINVRDL
|||||
QSNIEERYKIQSYSEYKDFWGNPLMYNKYYFNAGKNKSYIKLAKDSPVGEILTRSKYNQNSKYINVRDL
220 230 240 250 260 270 280
290 300 310 320 330 340 350 360
YIGEXFIIRKNSQSINDIVRKEDYIYDFNNGEWRVYIYFKKEEKLFLAPISDSDELNTIQTQIK
|||||
YIGEXFIIRKNSQSINDIVRKEDYIYDFNNGEWRVYIYFKKEEKLFLAPISDSDELNTIQTQIK
290 300 310 320 330 340 350 360
370 380 390 400 410 420 430
EYDEQPTYSQCLLFKKDESDTEGLGIRHFYESGIVFEYKDYFCISKWYLKVRKPYNKLKGCNQFI
|||||
EYDEQPTYSQCLLFKKDESDTEGLGIRHFYESGIVFEYKDYFCISKWYLKVRKPYNKLKGCNQFI
370 380 390 400 410 420 430
440
PKDEGWE
|||||
PKDEGWE
X

```

US-09-910-186a-8 (1-440)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score = 189 Optimized Score = 259 Significance = -1.15
Residue Identity = 38% Matches = 162 Mismatches = 221
gaps = 17 Conservative Substitutions = 26

```

10 20 30 40 50 60 70
MANKYNSBILNNIILNRYKNNLIDLSGKGVAKVEYDGVLELN--DKNQFKLTSSANSKIRVTQNONIIFNS
|||
RYESNHIDLSRYASKINIGSKYVDFPDKNQIQLFNLESSKIEVLKNAIYNS
X 10 20 30 40 50
80 90 100 110 120 130 140
VFLDFSVFWIRPKYKNDGIONYNHETIINCNNKNSGKISIRGNRIITWLDIDNGKTSVFFEVNIRE
: |||
MYENESTFWIRPKYFNSIS--LNNEYTIINCNNKNSGKISIRGNRIITWLDIDNGKTSVFFEVNIRE
60 70 80 90 100 110 120
150 160 170 180 190 200 210
DISEYNIRWFEVITNNLNAKIYINGKLESNTDIKIDREVIANGELIIFKLDGIDRTQFIWMKYFSIFNT
|||
NISDYINRWIFVTITNNLNNKSIYINGRLIDQKPIGNLGNHASNIMEFKLDGCRDTHRYIWKYFNLFDK
130 140 150 160 170 180 190
220 230 240 250 260 270 280
ELSQSNIERYKIQSYSEYKDFWGNPLMYNKYYFNAGKNKSYIKLAKDSPVGEILTRSKYNQNSKYINY
|||
ELNEKEIKLDYDNQNSGILDKFDYLDQYKPYMLNLYDPNPKYDVNNVNGIRGYMLKPGSGVMTNTIY
200 210 220 230 240 250 260
290 300 310 320 330 340 350
RLDIYGEKFIIRKNSQSINDIVRKEDYIYDFNNGEWRVYIYFKKEEKLFLAPISDSDELNTIY
|||
LNNSLYRGKFKFIKKYASGNKNDIVNRNDYINIVYKKNREYRLATNASQAGVEKILSALEIPDVGNLSQVY
270 280 290 300 310 320 330 340

```

```

360 370 380 390 400 410 420
QIKEYDQPTYSQCLLFKKDESDTEGLGIRHFYESGIVFEYKDYFCISKWYLKVRKPYNKLKGCNW
|||||
VHRSKNQGGI--THKCKANLQDNNGNDIGFICFHQFNIAKLV-----SNWYNRQIERS--SRTLGCSW
350 360 370 380 390 400
430 440
QFIKDEGWE
|||||
EFIPVDDGWERPL
410 X

```

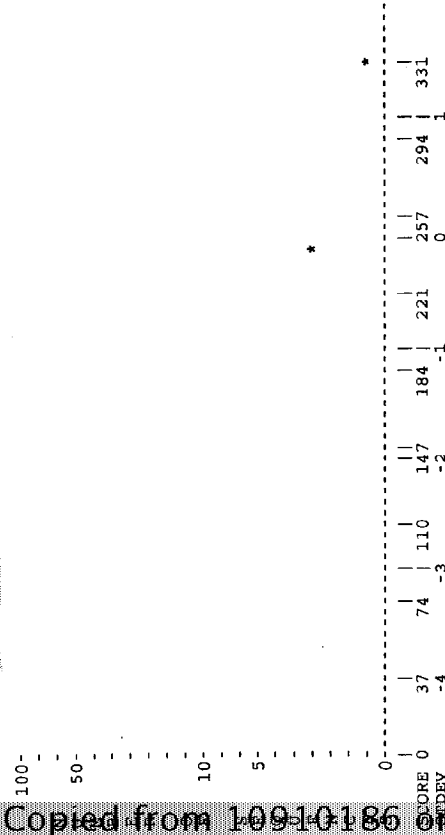
> O <
O: 10 Intelligenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-9.res made by bobyren on Thu 7 Nov 102 14:42:59-PST.

Query sequence being compared: US-09-910-186A-9 (1-1371)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-9 (1-1371) with:
File: US08123975A.seq



PARAMETERS

Unitary 1
K-tuple 4
Joining penalty 30
Window size 500
Similarity matrix
Mismatch penalty 5.00
Gap penalty 0.33
Gap size penalty 1
Cutoff score 0
Randomization group

SEARCH STATISTICS

Scores: Mean 270 Median 241 Standard Deviation 52.54
Times: CPU 00:00:00.00 Total Elapsed 00:00:01.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.		
**** 1 standard deviation above mean ****						
1. US-08-123-975A-6	Sequence 6, Application U	1351	331	618		
**** 0 standard deviation from mean ****						
2. US-08-123-975A-4	Sequence 4, Application U	1338	240	620		
3. US-08-123-975A-1	Sequence 1, Application U	1338	240	620		
**** 1 standard deviation below mean ****						
1. US-09-910-186A-9	(1-1371)					
1. US-08-123-975A-6	Sequence 6, Application US/08123975A					
Initial Score	= 331	Optimized Score	= 618	Significance = 1.16		
Residue Identity	= 50%	Matches	= 706	Mismatches = 545		
Gaps	= 138	Conservative Substitutions	=	0		
40	50	60	70	80	90	100
ACCCACAACTCCCTCTTGAAGGACATCATCAACAGTACTTCAACACATCAACGACTCCAGATCTCTGT						
ATGCGTTTCAACAATACAAATCCGAATCCCTGAACAA--TATCATCTCTGA	X	10	20	30	40	
110	120	130	140	150	160	170
CCCTGCAGAACCCGTAAGACACCTTGTGACACCTCCGTTACACCGGAGGTCTCGAGGAGGAGGACG						
ACCTGCGTTTCAAAAGACAAATCTGATCGATCTGCTGTTACGGTGTCTAAAGTTGAAGTATACGACGGTG						
50	60	70	80	90	100	110
TCCAGCTGAACCCCAATCTTCCATTCGACTTCAAGTGGTTCCTCCGGTGAGGACAGAGGTAAGGTCTATCG						
TTGAACTGAATGACAAAGAC--AGTTCAAACTGACCTCTTCGGCT-----AACTCTAAGATCCGCTG						
130	140	150	160	170	180	
TCACCCAGACGAGAGACATCGTACAACTCCATGTACGAGTCTCTCCATCTCTTGGATCAGATC-						
TTACTCAGAAATCAGAAATCATCTTCAACTCCGTTATTCCTGGACTTCTGTTCTTCTGATCCGCTATCC						
190	200	210	220	230	240	250
CGAAATACAGAACGCGGTATCCAGAAATACATCCCAATGAATACACCATCATCACTGCATGAAGAATA						
260	270	280	290	300	310	320
ACTCTGTTGGAAGATCTCCATCCGCGGTAAACGTTATCATCTGACTCTGATCGATATCAACGGTAAAGACCA						
330	340	350	360	370	380	390
AGTCCATCAACTTCTCTTACGACATCTCCCAACACGCTCTGTTAGACAA--GTTGTTCTTCTCACC						
AATCTGTTATCTTTCGAATACAAACATCCGTTGAAGACATCTCTGAATACATCAATCGGTGTTCTTCGTTACCA						
400	410	420	430	440	450	460
TCACCAACACATGATGGTAACTGAGATCTACATCAACGGTAAAGTCTGATCGACACCATCAAGTCTCAAGG						
TCACCAATTAACCTGA--AACTGCTAAATCTACATCAACGGTAACTGGAATCTTAATACCAACATCAAA						
470	480	490	500	510	520	530
AGTTGACCGGTATCAACTTCCCAAGACCATCACTTCGAGATCAACAGATCCAGACACCGGTCTGTATCA						
ACATCCGTGAAGTATTCGCTAACCGGTGAATCATCT-----TCAAACTGGACGGTACATCATCTGATCCC						
540	550	560	570	580	590	600
CCTCCGACTCCGACAAACATCAACATGTGGATCCGTGACTTCTATCTTCGCCAAGGAGTGTGACGCTAAG						

```

AGT-----TCTGTGATGAATATCTTCCATCTTCAACACCGAAGTCTTCTAGTCCA
610 620 630 640 650
740 750 760 770 780 790 800
ACATCAACATCCCTTTCAACTCTTTCAGTACACCAAGCTGTCAGGAGTACAGGAGTCTGAGAT
740 750 760 770 780 790 800
ATATCGAAGAACGGTACAGATCGATCTTACCTCCGATACCTGAGGAGTCTTCTGGGTATCCGCTGATG
660 670 680 690 700 710 720 730
810 820 830 840 850
ACAAAGAGGAGTACTACATGCTCAACATCGACTTGTGAACAGATACAT-----G
810 820 830 840 850
ACAAAGAGGAGTACTATCTATCTCAATGCTGCTGAAGAGTCTTACATCAAACTGAAGAAAGTCTCTCGG
740 750 760 770 780 790 800
860 870 880 890 900 910
TACGCCAATCTCCAGACAGTCTGTTTCAACACGAGAGT-----AACAAACGAGTCTCAAGAGG
860 870 880 890 900 910
TTGGTGAATCTCTGACTCGTTCCAAATACAAACAGAGTCTTAATATACATCAACTACCGGAGCTGTATCG
810 820 830 840 850 860 870
920 930 940 950 960 970 980 990
GTTACAGATCATCATCAAGGATACAGGATACAGGATACAGGATACAGGATACAGGATACAGGAT
920 930 940 950 960 970 980 990
GTGAAAGTTCATCATC---CGTGGCAATCTAATCTCTAGTCCATCA-----ATGATGATC---GT
880 890 900 910 920 930
1000 1010 1020 1030 1040 1050 1060
ACTTCGACATGACTATCAACAGAGGCTTACACCTGTTCTATGAGAGAGGAGGAGGAGGAGGAGG
1000 1010 1020 1030 1040 1050 1060
ACGTAAGAGAGACTA-CATCTACCTGACTCTTCTACCTGATACAGGAGGAGGAGGAGGAGGAGG
940 950 960 970 980 990 1000
1070 1080 1090 1100 1110 1120
ACTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
1070 1080 1090 1100 1110 1120
AGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
1140 1150 1160 1170 1180 1190 1200
AGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
1140 1150 1160 1170 1180 1190 1200
AGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
1080 1090 1100 1110 1120 1130 1140
1210 1220 1230 1240 1250 1260 1270
TCTCGGATCTGTTCCATCGGTACCTACAGATC-----CGTCTGGGTGGTGGTGGTGGTGGTGG
1210 1220 1230 1240 1250 1260 1270
CTGAGGAAATCGGTCTGATGCTGATCCACCGTTTCTACGATCTGATCTGATCTGATCTGATCTG
1150 1160 1170 1180 1190 1200 1210
1280 1290 1300 1310 1320 1330
ACTACTTGGT-TCCAACTG-----TCAAGAGGAGTAA---CTAGGCTCTCTGCTGGAGTCCACTTCCACCC
1280 1290 1300 1310 1320 1330
ACTTCTGATCTCCAAATGTTGATCTGAGGAGGAGTAAACCGCAACCGTACAACTGAACTGGGTTGCA---
1220 1230 1240 1250 1260 1270 1280
1340 1350 1360
ACTGGAGATCTGCTCC---AGTCTCCGAGTAAATAGGATTC
1340 1350 1360
ATTGGAGTCTATCCCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
1290 1300 1310 1320 1330 1340

```

2. US-09-910-186a-9 (1-1371)
US-08-123-975a-4 Sequence 4, Application US/08123975A

Initial Score = 240 Optimized Score = 620 Significance = -0.57
Residue Identity = 49% Matches = 686 Mismatches = 593
Gaps = 111 Conservative Substitutions = 0

```

CCATTCAACATCTTCTCTACACCAACTCCCTGT-TGAAGGACATCATCAACAGGATCTTCTCAACACAT
100 110 120 130 140 150 160
CTCGAGCCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
X 10 20 30 40 50
90 100 110 120 130 140 150 160
CAACGACTCCCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
CAACGACTCCCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
CATCAATACCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
60 70 80 90 100 110 120
170 180 190 200 210 220 230
GGTCTCCGAGGAGGAGTCCAGCTGAGTCCAGCTGAGTCCAGCTGAGTCCAGCTGAGTCCAGCTGAGT
GGTCTCCGAGGAGGAGTCCAGCTGAGTCCAGCTGAGTCCAGCTGAGTCCAGCTGAGTCCAGCTGAGT
AATCAACATCGGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAG
130 140 150 160 170 180 190
240 250 260 270 280 290 300
GGACAGAGGTAAGGTATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
GGACAGAGGTAAGGTATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
GGAATCTTCCAAATCGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
200 210 220 230 240 250 260
310 320 330 340 350 360
CTCTCTTGGATCAGATC---AACAGTGGGTCTCCACTTGC-----CAGGTTACACATCATCTGACT
CTCTCTTGGATCAGATC---AACAGTGGGTCTCCACTTGC-----CAGGTTACACATCATCTGACT
CTCTCTTGGATCAGATC---AACAGTGGGTCTCCACTTGC-----CAGGTTACACATCATCTGACT
270 280 290 300 310 320 330
370 380 390 400 410 420 430 440
CGTCAAGAACAACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
CGTCAAGAACAACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
CATGGAACAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
340 350 360 370 380 390 400
450 460 470 480 490 500
GGACTCCGAGGAGTCCACTTCTCTCTACGATCTCTCAACATCTCTGCTGCTGCTGCTGCTGCTGCTG
GGACTCCGAGGAGTCCACTTCTCTCTACGATCTCTCAACATCTCTGCTGCTGCTGCTGCTGCTGCTG
GGAATCAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
410 420 430 440 450 460 470
510 520 530 540 550 560 570 580
CTTGGTCAACGCTCAACCAACATGATGGGTACATGATGATGATGATGATGATGATGATGATGATGAT
CTTGGTCAACGCTCAACCAACATGATGGGTACATGATGATGATGATGATGATGATGATGATGATGAT
CTTGGTCAACGCTCAACCAACATGATGGGTACATGATGATGATGATGATGATGATGATGATGATGAT
480 490 500 510 520 530 540 550
590 600 610 620 630 640 650
CAAGGTCAAGGAGTTCAGGCTATCAACTTCTTCAAGACCATCACTTCTGATGATGATGATGATGATG
CAAGGTCAAGGAGTTCAGGCTATCAACTTCTTCAAGACCATCACTTCTGATGATGATGATGATGATG
ACCGATCTCCAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
560 570 580 590
660 670 680 690 700 710 720
CGGTCTGATCACTCCGAGTCCGACATCACTGATGATGATGATGATGATGATGATGATGATGATGAT
CGGTCTGATCACTCCGAGTCCGACATCACTGATGATGATGATGATGATGATGATGATGATGATGAT
TGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
610 620 630 640 650 660 670
730 740 750 760 770 780 790
GGACGCTGAAGGAGTCAACATCTCTCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
GGACGCTGAAGGAGTCAACATCTCTCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
GAACGAAAGAAATCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
680 690 700 710 720 730 740
800 810 820 830 840 850 860
CGACCTGAGATCAACAGAGGAGTACTATGATGATGATGATGATGATGATGATGATGATGATGAT
CGACCTGAGATCAACAGAGGAGTACTATGATGATGATGATGATGATGATGATGATGATGATGAT
CTACCTGAGATCAACAGAGGAGTACTATGATGATGATGATGATGATGATGATGATGATGATGAT
750 760 770 780 790 800 810
870 880 890
CAGACAGATCGTCTTCAAC-----ACCAGA-----CGTAAACAAACAGCTTCA-
870 880 890

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126 Copied from 10910186 on 05-05-2004

CATGATCGTACCGTATCTGGA---TGAATATCTTCTCATCTTCAACACCG---AAGTGTCTAGTCC
 600 610 620 630 640 650
 790 800 810 820 830 840 850
 GATGGTCTCATCAGCTTACCGTGTATGATCTTCACTTACCAATCATGTTTGTGGA---CGGTGAC
 860 870 880 890 900 910 920
 GAAGAACCACTTCTGTGTAACACGAGGCGTGTG---AGATGTGAGAGAGTGTGATGCACTCTCG
 930 940 950 960 970 980 990
 GAGTCCCTGCTTCTGCTTCAGGTTGAAGACACGAGAGTTGGAGATGATACCGATGACCAACCGGAGTTGTC
 1000 1010 1020 1030 1040 1050 1060
 TTGACGAGTCTGATGATGTTGTAACCTGCAAGTTGGAGACCCCACTTGTGATCTGATCCAGAGAGATG
 1070 1080 1090 1100 1110 1120 1130 1140
 GAGAGGACTCGTACATGAGTGTGATGATG---TCTCGTGTGGTACGATGACCTTACCTCTGCTTC
 1150 1160 1170 1180 1190 1200
 AAAGAGAGAAAGCTTTCCTGGGTCCGATCTGATTCGAGCACTTACACACCACTTACAGATCAAA
 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330
 GACCTCGGCTGTGTAACCGGAGGTGTCGACCAAGTGTCTT-----ACGTTCTGCT---AGGACA
 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500
 GATGCTGGAGTCTGATGTTGTAAGTACTCGTGTGATGATGCTTCAACAGGAG---TTGTTGGTGTAG
 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700
 CGGTCTGATCGGTATCCCGTCTTCTACGATCTGCTGATCGTATCGTATTCGAGATACCAAGACTTCTGCA
 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900
 1340 1350 1360 1370
 GAGAGATGTTGATG---GGATGTCATCGTGAATTC
 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500
 CTCCAATGTGATCTGAAGAGTTAAACCAACCGTACCACTGAACTGGGTTG
 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700

2. US-09-910-186a-9' (1-1371)

US-08-123-975A-4 Sequence 4, Application US/0812375A

Initial Score = 40 Optimized Score = 404 Significance = -0.54
 Residue Identity = 40% Matches = 485 Mismatches = 626
 Gaps = 91 Conservative Substitutions = 0

150 200 210 220 230 240 250 260
 TGAAGATCGGAACCGTAGTAAAGTGTGTTGATGCTGATGCTGGAAGATGATGTTGCTGTTGATG
 270 280 290 300 310 320 330
 CTCGAGCCATCGGCTCGTCTGCTACCTTCACTGAATACATCAAGACAT
 x 10 20 30 40 50

CCTTGTCTCTCACGACGACGATGGCGTAG-ATGTCTCGGTGGAGTG-ATTGTCGGCGTACATGATCTC
 60 70 80 90 100 110 120
 CATCAATCCTCCATCCTCACTGCGTACGATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAA
 130 140 150 160 170 180 190
 GTTCTTCATGACACAGGTTTGAAGCCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG
 200 210 220 230 240 250 260
 AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGCAAGAATCAAGATCCAGCTGT-----TCAA
 270 280 290 300 310 320 330
 TCTGTGTCTGTGTTTACCTCTGATACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT
 340 350 360 370 380 390 400
 TCTGTGTCTGTGTTTACCTCTGATACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT
 410 420 430 440 450 460 470
 TCTGTGTCTGTGTTTACCTCTGATACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT
 480 490 500 510 520 530 540
 ACCTGTGTGTTTGAAGACGATCTGCTGGAGTTGGGTACATGATGATGATGATGATGATGATGATGATGATG
 550 560 570 580 590 600
 GT-----AGTACTCTCTGTTGATCTCAGGTCGTTACCCCACT-AGTCTTGGACGCTTGTGTGTGATC-T
 610 620 630 640 650 660 670 680
 GCAAGGAGTTGACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
 690 700 710 720 730 740 750
 TCAATCGTGTGATCTGCTGATCCTTACCAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAA
 760 770 780 790 800 810 820
 TCTTGGAGAGTTGATACCGTCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 830 840 850 860 870 880 890
 TCAATGTT-ACCCATCATGTTTGTGAGCGGTGACGAGAACCACTTGTGTAACCAAGAGCGTTGTGTTGAG
 900 910 920 930 940 950 960
 ATGCTGTAGGAGAGTTGATGAGTCTGCTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
 970 980 990 1000 1010 1020 1030
 ATGATACCGATGACCAACCGAGTTGTTTCTGACCGAGTCTGATGATGATGATGATGATGATGATGATGATG
 1040 1050 1060 1070 1080 1090 1100 1110
 CACTTGTGATCTGATCCAGAGAGAGATGAGAGAGCTCTGATGATGATGATGATGATGATGATGATGATGAT
 1120 1130 1140 1150 1160 1170 1180 1190
 AATACGTTGA-CGTCAACAATGAGGTATCCGCGGTTATACATGATGATGATGATGATGATGATGATGATGAT
 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330
 TGGGT---GAGGATGACCTTACCTCTGCTCTACCGGAGGACCCCACTGATGATGATGATGATGATGATGATG
 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500

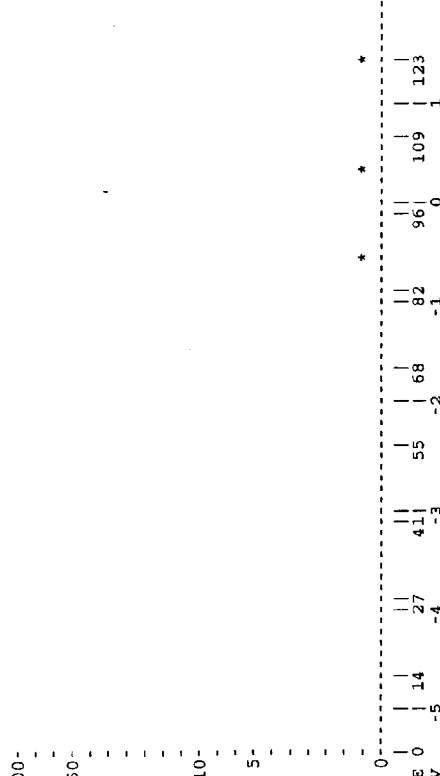
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-10.res made by bobryen on Thu 7 Nov 102 14:33:22-PST.

Query sequence being compared:US-09-910-186A-10 (1-450)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-10 (1-450) with:
File : US08123975A.pap



PARAMETERS

Similarity matrix PAM-150 k-tuple 1
Threshold level of sim. 16%
Mismatch penalty 1 Joining penalty 20
Gap size penalty 5.00 Window size 450
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 104 Median 89 Standard Deviation 17.56
Times: CPU 00:00:00.00 Total Elapsed 00:00:01.00

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Init. Opt. Frame

1. US-08-123-975A-2 Sequence 2, Application U 850 251 1.08 0
**** 1 standard deviation above mean ****
**** 0 standard deviation from mean ****
2. US-08-123-975A-5 Sequence 5, Application U 439 238 -0.06 0
3. US-08-123-975A-3 Sequence 3, Application U 415 88 229 -0.91 0

1. US-09-910-186A-10 (1-450)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score = 123 Optimized Score = 251 Significance = 1.08
Residue Identity = 25% Matches = 121 Mismatches = 286
Gaps = 28 Conservative Substitutions = 31

X 10 20 30 40 50
MTIPFNIFSYNNLSLLKDIINEYFNNDKSLQNRKNTLVDTSGYNAEV
KLYLIGSAEYKSKVKYKLTIMPDLSTVNTDILIEFNKYNSEILNLLRYKDNLLDLSGYGAKV
380 390 X 400 410 420 430 440

60 70 80 90 100 110
SEEGDVOLNPIFPDFKLGSGEDRGKVIIVTONIVNMYESISFWIRNKWSN-----LPGYTII
EYDGVNLNDKNOFKLTSSAN---SKIRVTQNONIIFNSVFLDFSVFIRIPKYNKDGIONYIHNEYTII
450 460 470 480 490 500 510

120 130 140 150 160 170 180 190
DSVFNNSGWSIGIISNLFVTLKQNEDESEQSNFSDISNNAPGYKWFVVTNNMGMKIYINGKLIDT
NCKMNSGKISIRGNRIIWTLDINGKTSVFEYFNREDISEYINRWFFVTITNNLNNAKIYINGKLESN
520 530 540 550 560 570 580

200 210 220 230 240 250 260
IKVKELGICNFSTIIFKINKIPDTGLITSDSNINWIRDFVIFAKELDGDNDINLENSLOYTNVVKDYWG
TDIKDIREVANGELIKLGDIDRTOF-----IWKYFSIFNTLSQSNIEERYKIQSYSLKDFWG
590 600 610 620 630 640

270 280 290 300 310 320 330
NDLRNKEYYMNVDYLNRYMYANSROIIVENTRRNNDNEGYKIIKIRGNTNDRVRGDDILYFDMTIN
NPLMYNKEYYMFNAGNSYKLLKDPVCEILTRSKYNSKYNRYDLYIGKEFLIIRKNSOSINDDIV
650 660 670 680 690 700 710 720

340 350 360 370 380 390
NKAYNLFMKNETM-----YADNHSTEDIYAGLREOTKDINDNIIFQIOPMNNYTYAQAIFKSNFNGE
RKEDYIYLDFFNLNQEWRYTYKYFKKEEKLFLAPISDSDFYNTIOIKEYDEQPTYSCOLLKXDESTD
730 740 750 760 770 780 790

400 410 420 430 440 450
NISGICSTGYRFLRGDWRHNYLVT--VKQNTYASLLESTHWGFVPVSE
EIGLIGHRFYESGIVFEYKDYFCISKYWLKVKRPPYNLKLGCNQFIPKDEGWTE
800 810 820 830 840 X 850

2. US-09-910-186A-10 (1-450)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 103 Optimized Score = 238 Significance = -0.06
Residue Identity = 25% Matches = 115 Mismatches = 274
Gaps = 28 Conservative Substitutions = 30

10 20 30 40 50 60 70
MTIPFNIFSYNNLSLLKDIINEYFNNDKSLQNRKNTLVDTSGYNAEVSEGDVOLLNPIFPDFKLG
FNKYNSEILNLLRYKDNLLDLSGYGAKVEYDGVNLNDKNOFKLTSSA
X 10 20 30 40 50

	270	280	290	300	310	320
--	-----	-----	-----	-----	-----	-----

12-09-010-1862-10 17-4501

113-00-010-1862-10 (1-450)

total Score	=	88	Optimized Score	=	229	Significance	=	-0.91
idue Identity	=	27%	Matches	=	117	Mismatches	=	251
s	=	32	Conservative Substitutions	=	30			

LKDINFEYNNDSKILSLQNKNTLVDTSYNAEVSSEGVQLNPFDFPKLSSGSDRDKVITTONEN
 : : : : :
 RYESNHLDLSRYASKINIGIKSVNFDPIDKNQIOL--FNLESSKIEVLKNA
 X 10 20 30 40 50 60 70 80

[illegible]

160 SNNAPGV-NKWFVVTNNMGNKKIYINGKLIDITKYKEITGTFNSKTIFEINKIPDPTGLTISDSDNINM
170 :
180 :
190 :
200 :
210 :
220 MINISDYINRWKFVTNNLNNSKVIYNGRLIDOKPITPSNLGNTHASNNIMFKLDGGCDT-----HRYI

```

      230       240       250       260       270       280       290
WIRDFYFAKELDGKDINILFNLSQYTNNVGVNDLRYNKEYEYNMIDLYNMYSRQI-----
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
WIKTFNFDELNEKEKKDIYDQNQSGLKFWDGDTLOYDKPYMYMLNLDPNKYVDNVNGTGYMWLKGP

```

```

300      310      320      330      340      350
----VFVTRRRNNDFEGYKIIKIRGRGNTNTRVGGDILFYDMTINKAYNFEMKNWTYADNHSIEDIY
RGSVTTNIVNSSLVSGTGFELIKKYASGNKDNIVNRNDRVYINVVKNKEVRL-----ATNAAOAGVEKIL

```


2. US-09-910-186A-11 (1-1374)

```
Initial Score      = 454  Optimized Score = 624  Significance = 0.59
Residue Identity  = 50%  Matches          = 669  Mismatches   = 619
Gaps              =    49  Conservative Substitutions = 0
```

CCATTCAACATCTTCTCTCACCCACACACTCCTTGTG-TGAAGGACATCATCAAGCATGACTTCTCAATCCGAT

[illegible]


```
CTTGCCAGCTGCTGTTCAAGAAAGATGAAGAACTTACTGACGAAATCGGCTGATCGGTATCCACCGTTTCT
1110 1120 1130 1140 1150 1160 1170 1180
1240 1250 1260 1270 1280 1290 1300
AAGCCTTGGCGTTTCTCCTTCAAGAGCGCTACACTCCCTGTGCGCTACCAACTACGAGACCAAG-----
| | | | | | | | | | | | | | | | | |
ACGAATCTGTTATCGTATTGCGAAGAAATACAAAGACTACT-TCTGCATCTCCAAATGGTACCTGAAGGAAGTT
1190 1200 1210 1220 1230 1240 1250
1310 1320 1330 1340 1350 1360
-----CTGCTGTCCACC-----TCCTCCTTCTGGAAGTTGATCTCCCGTGACCCAGGTTGGGTCGAG
| | | | | | | | | | | | | | | | | |
AAACGCAACCGTACAAACCTGAACACTGGGTTGCAATTGGCAGTTTCATCCCGAAAGACGAGGTTGGACCGAA
1260 1270 1280 1290 1300 1310 1320
1370 x
TAATAGGAATTC
| | | |
TAGTAACCTCTAGAGTCGAGGCGCTGCAG
1330 x 1340 1350
```


Copied from 10910186 on 05-05-2004

CTCAGCCATGGCTCGTCTGCTGTCTACTCTTCACTGAATACATCAAGAACAT	150	160	170	180	190	200	210
X	10	20	30	40	50		
TAAGTCCTCTCCGTTTTTAACATGAGATACAGAATGATAAATACGTCCGACTTCGGTTCAGGACTCGAA	220	230	240	250	260	270	280
	60	70	80	90	100	110	120
CATCAATACCTCCATCTCTGAACTCGCGTTCGAAATCCCAATCACTGATCGACCTGTCTCGCTACGGTTCGAA	290	300	310	320	330	340	350
	130	140	150	160	170	180	190
TATCAACATTAAAGGTGACGTGTACAAGTACCCAACTAACAAAAACCAATTCGGTATCTTCAACACGACAAGCT	360	370	380	390	400	410	420
	220	230	240	250	260	270	280
AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGATCAGATCCAGCTGTTCATCTCGGAATC	290	300	310	320	330	340	350
	130	140	150	160	170	180	190
TTCCGAGGTCAACATCTCTCAAAACGACATACATATCTACGACAAACAGTAAAGAACTTCTCTATTCTTT	360	370	380	390	400	410	420
	220	230	240	250	260	270	280
TTCCAAAATCGAAGTTATCTCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACTCTT	290	300	310	320	330	340	350
	200	210	220	230	240	250	260
CTGGTCCGATCCCGAAATACTTCAAC---TCCATCTCTCTGCAACATGAATACACCATCATCTCACTGCAT	360	370	380	390	400	410	420
	270	280	290	300	310	320	330
GAGAGACAAACACTCCGGTTGGAAGTCTCTCTTAAACCAACGAGATCATTTGGACCTTGCAGAACACAGC	430	440	450	460	470	480	490
	430	440	450	460	470	480	490
G---GAAACAATCTCGTTGGAAAGTATCTCTGAACTACGGTGAATCATCTGGACTCTGCAGACACATCTCA	340	350	360	370	380	390	400
	340	350	360	370	380	390	400
AGGTATTAAACCAAAAGTTAGCATTTCAACTACGGTAAACCAACGGTATTTCTGACTACATCATCAAGTGGAT	510	520	530	540	550	560	570
	510	520	530	540	550	560	570
GGAAATCAAAACACGCGTTGTATTCAAAATCTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGAT	410	420	430	440	450	460	470
	410	420	430	440	450	460	470
TTTCGTCACTCACTCACTAAGCAGATAGGTGACTCTAAGCTTTACATTAACGGTACTTAATCGACCAAAA	580	590	600	610	620	630	640
	580	590	600	610	620	630	640
CTTCGTTACCATCACCACAACAATCGTCTGAAATTAATCTCCAAAATCTACATCAACGCGCGTGTGATCGACCA	480	490	500	510	520	530	540
	480	490	500	510	520	530	540
GTCCATTTTAACTTAGGTAACATTCACGTTTCTGACAAACATCTATTCAAGATCGTTAACTGCAGTTACAC	650	660	670	680	690	700	710
	650	660	670	680	690	700	710
ACCGATCTCAATCTGGTTAAATCCACGCCTCTAATTAACATCATGTTCAACTGGACGGTGTGCTGTGACAC	560	570	580	590	600	610	620
	560	570	580	590	600	610	620
---CAGATACATTGGATTAGATACCTCAACATTTTCGACAAGAGTTAGACGAGACCGAGATTCACAACTTT	720	730	740	750	760	770	780
	720	730	740	750	760	770	780
TCACCGCTACATCTGGATCAAAATCTTCAATCTGTTCGACAAGAATCTGAACGAAAAAGAAATCAAGAAGCT	630	640	650	660	670	680	690
	630	640	650	660	670	680	690
ATACGACAACGACCTTAACACCAATATTTTGAAGGACTCTGGGGTAACCTACTTGTCTTACGACAGGAATA	790	800	810	820	830	840	850
	790	800	810	820	830	840	850
GTACGACAACCGATCCAAATCTTGGTATCTCTGAAAGACTCTTGGGGTGACTACCTGACGTACGACAAACCGTA	700	710	720	730	740	750	760
	700	710	720	730	740	750	760
CTACTCTGAATCTGTAGATCCGACAAATATACGTTGACGCTCAACAATGTAGGTATCCCGGTTACATGTTA	860	870	880	890	900	910	920
	860	870	880	890	900	910	920
CTACTATTAAACGCTTAAACCCCAACAACTTCAATGA---TAGAGAAGGATCTTACTTTAGCATTA	930	940	950	960	970	980	990
	930	940	950	960	970	980	99

2. US-09-910-186A-13 (1-1400)
US-08-123-975A-1 Sequence 1, Application US/08123975A

```
Initial Score      = 427  Optimized Score = 592  Significance = 0.58
Residue Identity = 54%  Matches      = 739  Mismatches  = 539
Gaps              = 72  Conservative Substitutions = 0
```

70 80 90 100 110 120 130 140
TCCCTTTTAAGCTTTCCTTCTTATACAGATGATAAAATTTTAATTTCCCTACTTCAACAAGTTCTTCAAGAGAAAT

```

CCTGAAAGGTCGCGGTGTTCTGTATGACTACCAATCTACCTGAACTCTTCCCTGTACCGTGGTACCAA
840 850 860 870 880 890 900 910
GGTTAAGATCAAGAGATTAAACACTCTCTACTACGATACCTTGTTAGAAAGACGATCGGTCTATAT
920 930 940 950 960 970
ATTCTATCAAGAAA---TACGGCTGTGTAACAGGACATATGTTTCGCAACAATGATCGTGTATACAT
980 990 1000 1010 1020 1030 1040 1050
TAATCTCGTGCCT---AGCAAGACTCACATATATCCCAATTA---TATGCTGATACCGCTACCAACCAAGGA
1060 1070 1080 1090 1100 1110 1120
GAAGACCATCAAGATCTCTCTCTGCAACAGATTAACCAAGTCTGCTGTTATGAATCC-----
1130 1140 1150 1160 1170
GTCTGCTGTAAGTAAACCAAGAAATACCGTCTGGTACCAATGCTTCTCAGCGCTGGTGTAGAAAAGATCTT
980 990 1000 1010 1020 1030 1040 1050
GTTGGAAGATCTCCATCCCGGTAACCGGTATCATCTGACCTGTATATCAACGGTAAAGCAAAATCTG
340 350 360 370 380 390 400
450 460 470 480 490 500 510
GTGGAAGGCTCTCTTTAACCAACAGAGATCATTTTGGACCTTGCAAGAACAGCGAGTTTAAACCAAGT
520 530 540 550 560 570 580
TAGCATTTCAACTACGTTAGCGCAACGGTATTTCTGACCTACATCAACAGTGGATTTTCGTCNCTATCACTA
590 600 610 620 630 640 650 660
ACGACAGATTAGTGTGACTCTTAAGCTTTTACATTAACGTTAACTTAATCGACCAAAAGTCCATTTTAACTTAG
670 680 690 700 710 720 730
GTAACTTACGTTTCTGACAACTCTTATTCAA---GATCGTTAACTGACGTTACACGAGATCATATTGGCA
740 750 760 770 780 790 800
TTAGATCTTCAACATTTTCGACAAAGGATTAGACGACGACGAGATTCAAACTTTTATACAGCAACGAACCTA
810 820 830 840 850 860 870
ACACCAATATTTTGAAGACTTCTGGGTAACCTACTTGTGTTACGACAGGAAATACCTACTTATTAAAGCTGT
880 890 900 910 920 930
TAAAGCCAAACACTCTCATGTATGATGAGGAAAGATTTCT-----ACTTTAAGCATTTAAACACATC
940 950 960 970 980 990 1000
AGAGGACACTATCTTTTACTA---ACAGATTATCTCTGTTATCAAGGTTAGATCCAAAGAGTTAAACA
1010 1020 1030 1040 1050 1060
ACTCT---TCTACTAAGCACTGTTTGAAGAAAGCAAGTACGAGTGTATATTAACCTTCGCTGAGCAAGA
1070 1080 1090 1100 1110 1120
CTCACTTATTTCCCATTTATGTTGATACCGCTACCAACCAAGGAGAGACCATC-----AAGAT
1130
ATCAGGAATGCG--GTGTATACACCTTACAGTACTTTCAGAGAGAGAGAAAGCTTTTCTCGCTCCGAT
980 990 1000 1010 1020 1030 1040
CTCCTCTCTGGCAACAGATTAAACCAAGTCTGCTGTATGAACCTCCGTCG-----GTAACACATCTACCAT
1140 1150 1160 1170 1180 1190

```

```
CTCTGATTCCGACGAAGTCTACACACCATCCAGATCCAGAAATACGACGACACGCGACCTACTCTTGCCA
1050 1060 1070 1080 1090 1100 1110
1200 1210 1220 1230 1240 1250 1260
GAACCTTAAATAATAATGGAATAATTTGGTTGTAGTTTCA-AGGCAGATACTGTAGTTGCTAGTA
| | | | | | | | | | | | | | | | | |
GCTGCTGTTCAAGAAGATGAAGAAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATC
1120 1130 1140 1150 1160 1170 1180
1270 1280 1290 1300 1310 1320 1330
CTTGTGTTATTATACCCACA--TGGAGATCACCACCAACAGC-----AATGGATGTTTGGAACTTTATTCTTG
| | | | | | | | | | | | | | | | | |
TGGTATCGTATTTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAGTTTAAACGCAA
1190 1200 1210 1220 1230 1240 1250
A-----AGAACATGGATGCAA--GAAAAATAATAGGATCCGGCGCGCGACGCGTCCCGGACTAG
| | | | | | | | | | | | | | | | | |
ACCGTACAACTGAAGTGGTTGCAATTGGCAGTTCTATCCCGAAGACG-----AAGTTGGACCGAATAG
1260 1270 1280 1290 1300 1310 1320
1340 1350 1360 1370 1380 1390
A-----AGAACATGGATGCAA--GAAAAATAATAGGATCCGGCGCGCGACGCGTCCCGGACTAG
| | | | | | | | | | | | | | | | | |
ACCGTACAACTGAAGTGGTTGCAATTGGCAGTTCTATCCCGAAGACG-----AAGTTGGACCGAATAG
1260 1270 1280 1290 1300 1310 1320
1400
TGAATTC
| | |
TAACCTCTAGAGTCGAGGCGCTGCAG
1330 X 1340 1350
```


TAAGTAGTATTCCTTGTCGTAAGCAAGTAGTACCCCAAGAGCTCTCAAAATATGGTGTTAGGTTGGTT

AAATCGTATTTCTTCGAATACAACATCCGCTGAAGACATCTCTGAATACATCATCGGTG - GTTCTTCGTTA

TAACACGTTTAAATAGTAGTATTCCTTGTGCTAAACAAAGTAGTTACCCAGAGCTCCTTCAAAATATTGGT
|||||
CATCACCATAATCACTGAACAATCTTAATAATCTACATCAACGCTTAACCTGGATCTAATACCGACATCAAGA
470 480 490 500 510 520 530
600 610 620 630 640 650 660
GTTAGGTTCTTGTCTGTATTAAGTTTGAATCTCGGTCTCGTCTTAACCTCTTGTGCAAAATGTTGAAGTATCT
|||||
CATCCGTGAAGTTATGCTGAACGTTGAATC-----ATCTTCCATCTTCAACCCGAACTGTCTCAGTCCAAATATCGAGA
540 550 560 570 580 590 600
670 680 690 700 710 720 730 740
AATGCCAATGTATCTGCTGTAACCTGAGTATGATCTGTAATAGATGTTGTCTAGAACCTGAAATGTTACC
|||||
-----CAGTTCACTCTGATGAAT--ACTTCTCCATCTTCAACCCGAACTGTCTCAGTCCAAATATCGAGA
610 620 630 640 650 660
750 760 770 780 790
TAAGTTTAAATAGGATTTTGGT--CGATTAGTTA-----CGTTAATGTAAGCTTAGA
|||||
ACGGTACAGATCCAGTCTTACTCCGAATACCTGGAAGACTTCTGGGTATTCGCTGATGTATCAACAAGA
670 680 690 700 710 720 730 740
800 810 820 830 840 850 860
GTCACCTAATCTGCTGTAAGTATGATGACGAAATCC--ACTGTGTGATGTAGTCAGAAATACCGTTGGC
|||||
-----ATACATATGTTCAATGCTGTATACAGACTCTTACATCAACTGAAAGAACTCTCCGGTTG--
750 760 770 780 790 800
870 880 890 900 910 920 930
TTACCGTAGTTGAATCTAATCTTGTGTTAATACCTGC--GTTGTCTTGCAGGTGCCAAATGATCTCGTTGTG
|||||
-----GTGAATCTGACTGCTCCAAATACACACAGAACTCTAATACATCACTACCGGACCTGTA
810 820 830 840 850 860
940 950 960 970 980 990 1000
GTTAAGAGACACTTC--CAACCGGAGTTGTTGT--CTCTCATACAGTTGATGATGATGATCTCGTTGTTAA
|||||
CATCGGTGAAGTTTCAATCATCGTCGCAAACTTAACTCTCACTCTAGTCCATCAATGA--TGACATGTAAGTAA
870 880 890 900 910 920 930
1010 1020 1030 1040 1050 1060 1070
CGTTGACGATCTTGTGCTGTAAGTAATCTCTACCCAGAAAGAAATAGAGAAGTTCTTGTACTTGTGT
|||||
AGAAAGACTA--CATCTACCTGGACTCTTCAACCTGAATCAGGAATGGGTGTATACACCTACAAGTACTTCA
940 950 960 970 980 990 1000
1080 1090 1100 1110 1120 1130 1140
CGTAGATAATGTAAGTCTGTTGAGAGATGTTGACCCGGAAGCTGTGCTGTGTAGATACCGAATGTTTT
|||||
AGAAAGAGAGAAAGCTTTTCTCGCTCCGATCTCTGATTCGACGAACTCTACAACACCATCCAGATCA
1010 1020 1030 1040 1050 1060 1070 1080
1150 1160 1170 1180 1190 1200 1210 1220
TGTTAGTTGGTACTTGTACACTCACCTACCTTAATGTTGATATGGAGTCGTAACCGAA--GTGTCCGAGTAT
AGNATACGACGACGACGACGACCTACTCTTCCAGCTGTGTTCAAGAAAGATGAAGATCTACTGACGAA
1090 1100 1110 1120 1130 1140 1150
1220 1230 1240 1250 1260 1270 1280 1290
TTATCATCTTGTATCTCATGTTTAAACGGAAGAGACTTAATCTCTTGAAGAACTGTTGAAGTAGGAA
|||||
TCGCTCTGATCGTATCCACCGTTTCTACAGATCTGATCTGATCTTCCAGAAATACAAAGACTACTTCTGCA
1160 1170 1180 1190 1200 1210 1220
1300 1310 1320 1330 1340 1350 1360
ATTAAATTTTATCATCTGTATGAAG--AAAGCTTAAAGGAATACTATTATTAGGTTACTAGTTACCAT
|||||
TCTCCAA-----ATGGTACCTGAAGAGTTAAACGCAACCGTACAACTGAACTGGTTGCATTTGGCAG
1230 1240 1250 1260 1270 1280 1290
1370 1380 1390 1400
AGAAATTAG--TTCTGTGCTGACTCTCTCCCTGGTGAATTC

TTTCATCCCGAAAGACCAAGTTGGACCGAATAGTAACTCTTAGAGTCCGAGGCTCGCAG
1300 1310 1320 1330 X 1340 1350

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file us-09-910-186a-14.res made by bobyen on Thu 7 Nov 102 14:34:07 -PST.

Query sequence being compared:US-09-910-186A-14 (1-449)
 Number of sequences searched: 3
 Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-14 (1-449) with:
File : US08123975A.pep

[illegible]

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	init. Opt.	Sig. Frame
1. US-08-123-575A-5	Sequence 5, Application U	439	158	247	0.58
2. US-08-123-575A-2	Sequence 2, Application U	850	158	271	0.58
	*** 1 standard deviation below mean ***				
3. US-08-123-575A-3	Sequence 3, Application U	415	143	276	-1.15

1. US-09-910-186A-14 (1-449)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score	=	158	Optimized Score	=	247	Significance	=	0.58
Residue Identity	=	31%	Matches	=	141	Mismatches	=	233
Gaps	=		Conservative Substitutions	=	35		=	34

20	30	X	40	50	60	70	80
NNNSIPKLSSTDDKILISVFNKFRKSSSVLNMRYKNDKVDVSGVDSNININGOVYKPYTNKKNQFIY							
FKRYNSEFRIINILNRYKONNLDISGYGAKVEYDGV--ELNDKNQKFLT							
X	10	20	30	40	50		
90	100	110	120	130	140	150	
NDKLESEVNISSNDYIYDANKRNFSGISFWIRPYDKNYV--VNNETIINCMDNRNKGWKSLSNEIIV							
SSANSKIRVTQNIQNFNSVFLDFSQVSWIRPYKNDQNIWHNEYIINCML--NNSGKKSIRGNCNLIIV							
60	70	80	90	100	110	120	130

160		170	180	190	200	210	220	230
TLODNACINOKLAFNYCNGANGSDYINKWIFVTIINDRLGSKLYINGNLIDQKSLINLGNIHVHSDNILEFKI								
			:		:		:	
TLIDNGKTSVFEYNIREHDISEYNRRFFVTIINN-LNNAKIYINGKLBSNTDIDKDREVTANGELIFKL								
130	140	150	160	170	180	190	200	210

240 250 260 270 280 290 300
-VNCSTYRIGIRWFNIFKDETEITLTSNFNNILKDQWGNLYIDREYLLNLVKPNNFDRRRS
 : : : : :
DGDIDRFQIMWKYFIETLSQSNIERKYOSSEY.KDFWGPNLMYKNREYFMAGNKSYIKLKDS
200 210 220 230 240 250 260
310 320 330 340 350 360

```

430      440      X
-----HTNSNGCFWNFISEEHGWQEK
      ||| ||| : |||
KWLKKEVRKPYNLKLCNWFQIPKDEGWE
410      420      430      X

```

2. US-09-910-186A-14 (1-449)
US-08-123-975A-2 Sequence 2. Application US/08123975A

```
Initial Score      = 158  Optimized Score = 271  Significance = 0.58
Residue Identity  = 32%  Matches      = 155  Mismatches = 254
GAPS              = 35  Conservative Substitutions = 35
```

	X	10	20	30	40	50
DEDFDNLKKNLLNYDENKYLIGSREYKSKVNYLKTIMPFOLSIYTDLTILMFKYKYNSEILNNIILNL	360	370	380	390	400	410
						420
:	:	:	:	:	:	:
MGESQOELNSWVTDTLNSIPFVLLSYTDDKILISYFNKFFKRIKSSVLLNM						

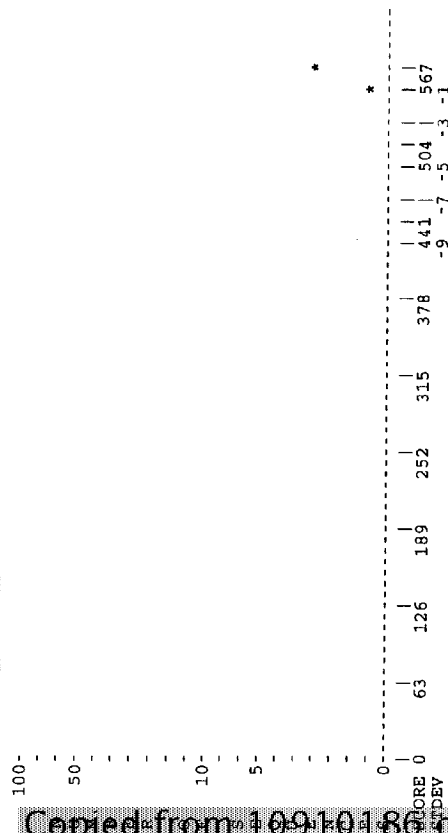
> O <
O/ O <
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-15.res made by bobryen on Thu 7 Nov 102 14:45:08-PST.

Query sequence being compared: US-09-910-186A-15 (1-1317)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-15 (1-1317) with:
File: US08123975A.seq



PARAMETERS

Unitary	4
K-tuple	30
Joining penalty	500
Mismatch penalty	5.00
Gap size penalty	0.33
Gap size	1
Cutoff score	0
Randomization group	

SEARCH STATISTICS

Mean	558	Median	542	Standard Deviation	15.01
CPU	00:00:00.00	Total Elapsed	00:00:00.00		

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	567	777	0.60	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	567	777	0.60	0
3. US-08-123-975A-6	Sequence 6, Application U	1351	541	675	-1.13	0

1. US-09-910-186A-15 (1-1317)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 567
Residue Identity = 60%
Gaps = 59
Optimized Score = 777
Matches = 813
Significance = 0.60
Substitutions = 473
Mismatches = 473

```

10  X 20 30 40 50 60 70
GAATTCAGATGTCCTACCAACGACAGATCCTGATCTGTACTTCAACAAGCTGTCAAGAAGATCAAG
CTGAGCATGGCTCG--TCTGCTGTCTACTTCACTGAATATACATCAAGAAGATCATC
X 10 20 30 40 50
80 90 100 110 120 130 140
GACAACTCCATCTTGGACATGATACGAAACAAATAAGTTCATCGACATCTCCGTTACGGTTCCAAATC
AATACCTCCATCTTGAACCTGCGCTAGCAATCCAAATCACCTGATCGACCTGTCTCGCTAGCTTCCAAATC
60 70 80 90 100 110 120
150 160 170 180 190 200 210
TCCATCAACGCTGCTCAGAACAGCATCATCTACAACGAGATACAGACATCTCTCCATCTCTCTTGG
GAGTCAACATCGCTCAGAACAGCATCATCTACAACGAGATACAGACATCTCTCCATCTCTCTTGG
AAATCCAGTTCCTTGAGATGCTATGTTACAACTCTATGTCGAAACATCTCTCCATCTCTCTTGG
210 220 230 240 250 260 270
280 290 300 310 320 330 340
GTCGGTATCCCAAGTACTTCAACAGGTCAACTGAATAACAGTACACCATCATCGACTCCGCTAAC
ATCGTATCCGGAATATCTCACTCCATCTCTGACAAATGATACACCATCATCACTGCATCGGAAAC
280 290 300 310 320 330 340
370 380 390 400 410 420 430
AATACTCCGATGGAAGATCTCCCTGAACTACAACAGATCATCTGGACCTGACGACCGCGGTAAAC
AAT---TCTGGTGGAAAGTATCTCTGAACTACGGTGAATCATCTGACTCTGCAGGACATCAGGAATC
350 360 370 380 390 400 410
440 450 460 470 480 490 500
AATCAGAAGTGGTCTTCAACTACCCAGATGATCTCCATCTCCGACTACATCAAGTGGATCTTCGTC
AAACAGCGTGTCTATTAATAATCTCTCAGATGATCAACATCTCTCAGTACATCAATCGCTGGATCTTCGTT
420 430 440 450 460 470 480
510 520 530 540 550 560 570
ACCATCAACAACTGCTGTAATAACTCAAAATCTAGATCAAGCGCGGTCTGTCGACGAAACCGATC
490 500 510 520 530 540 550
580 590 600 610 620 630 640
TCCAACTTGGTACATCCAGCTCCGACACATTTTGTCAAGATCTCGTGTGTAACGACAC---CCGT
TCCATCTGGTAACTACATCCAGCTTCTAATAACATCATCTTCAAACTGACGCGGTGTGTAACATCACC
560 570 580 590 600 610 620
650 660 670 680 690 700 710
TACGTCGGGATCGTTACTTCAAGTCTTCGACATCTGTTGGTGAACCGAGATCGAGACCTTGTACTCC

```


[illegible]

total score	=	541	Optimized Score	=	675	Significance	=	-1.13
idue Identity	=	54%	Matches	=	734	Mismatches	=	529
s	=		Conservative Substitutions	=	90		=	0

20	30	40	50	60	70	80	90
CCAACGACAAGATCCTGTGATCTTGTACTTCAACAAGCTGTACAAGAAGATCAAGGACAACACTCCATCTTGGACAC							
	ATGCGTTTCAACAAATCAAAATTCGGAATTCCTGGAATATCTGNAACAATATCATCTCGTGAACG						
	x	10	20	30	40	50	
100	110	120	130	140	150	160	
TGAGATACGAAACAATAAGTTTCATTCGACATCTCCGGTTTACGGTTCCACACATCTCATCAACAGGTGACGGTCT							
	TGCGTTTACAAGAACAACAATCTGATCGATCTGTCTGGTTACGGTGTCTAAAGTTGAAGTATACGACGGTGTGTG						
	60	70	80	90	100	110	120
170	180	190	200	210	220	230	
ACATCTACTCCACCAATPAGAAACAAGTTCGGAATCTACTCTCCACAGCCTTCGAGGCTCAACATCGGCTCAGA							
	AACT-----GAATGACAGAACCAAGTTTCAAAATGACCTCTTCGGCTAAACTCTTAAGATCCGGTGTACTCAGA						
	130	140	150	160	170	180	190
240	250	260	270	280	290	300	
ACAAGGACATCTCTACAAGGAAGATACCAAGAATCTTCATCTCTCTGGTCCGGTATCCCAAAAGTACT							
	ATCAGACACATCTTCAACTCCGGTATCTCTGGACTCTCTCTGTTCCCTCTGGATCCGGTATCCCGGAATACAA						
	200	210	220	230	240	250	260
310	320	330	340	350	360	370	
TCAAACAGGTCACCTTGAAT-----AACGAGTACACATCATCGATGATCCGTTAACAATAACTCCGG							

TCGCTGTTCAAGAAAGATCAGAGAACTTACTGACGAAATCGGFTCTGATCCGCGATCCACCGGTTCTTCTACGAATCTG	1120	1130	1140	1150	1160	1170	1180
1210	1220	1230					
GTGCGTCTCCTCTGG--TACTACAGAACATCCG-----							1240
GTATCGTATTCCGAAGATACAAAGACTACTTCTGCATCTCCAAATGGTACTCTGAGGAAAGTTAAACGCAAAAC	1190	1200	1210	1220	1230	1240	1250
1260							
1250	1260	1270	1280	1290	1300	1310	
CTCTCAAC-----GGTTGCTCTGTGGCTTCATCTCCAGGAGCACGGTTGCAGAGAACTATATAGG							
CGTACAACCTGAACTGGGTTGCATATGCGAGTTTCATCCCGAAGACGAAAGTTGCAGCGGAATAGTACCTC	1270	1280	1290	1300	1310	1320	1330
x							
AAATTC							
TAGAGTCGAGCCCTGCAG							
1340	1350						

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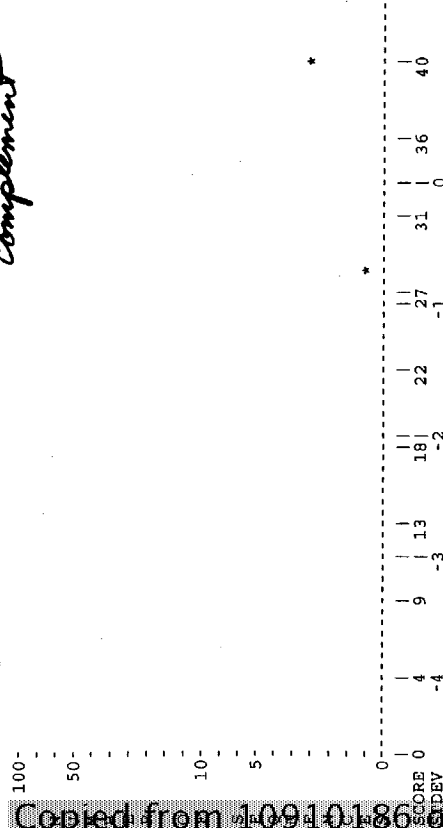
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-15-inv.res made by bobryen on Thu 7 Nov 102 14:45:24-PST.

Query sequence being compared: US-09-910-186A-15' (1-1317)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-15' (1-1317) with:
File: US09123975A.seq

Complement



PARAMETERS
Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap size penalty 5.00 Window size 500
Gap size penalty 0.33
Gap size penalty 0.33
Randomization group 0

SEARCH STATISTICS
Mean 36 Median 29 Standard Deviation 6.93
CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig.	Frame

1. US-08-123-975A-4 Sequence 4, Application U	1338	40	336	0.58	0	
2. US-08-123-975A-1 Sequence 1, Application U	1338	40	336	0.58	0	
**** 1 standard deviation below mean ****						
3. US-08-123-975A-6 Sequence 6, Application U	1351	28	200	-1.15	0	

1. US-09-910-186A-15' (1-1317)						
US-08-123-975A-4 Sequence 4, Application US/08123975A						
Initial Score = 40	Optimized Score = 336	Significance = 0.58				
Residue Identity = 40%	Matches = 409	Mismatches = 518				
Gaps = 74	Conservative Substitutions = 0					

TCTGGTGGAAAGTATCTCTGAACTACGGTCAATCATCTGGACTCTG-----CAGGACACTCAGCAATC						
350	360	370	380	390	400	410
X GAATTCCTATTAGTTCCTCCGCCAACCGTCTCTCTGGAGATGAAGGACGAG						
	10	20	30	40	50	
AAACAGCGTGTGTGTTTAAATCACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTGTT						
60	70	80	90	100	110	120
AAACAGCGTGTGTGTTTAAATCACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTGTT						
120	130	140	150	160	170	180
TGGAAACCCCAACAAACCGATGTTTCCACCGTGTGTGTTTGGAA-----GTTTCATGGTACAG-----TTATT						
180	190	200	210	220	230	240
ACCATCACCAACATCTCTGAATCACTCCAAATCTATCAACGCGGCTCTGATCGACCAAAACCGATC						
490	500	510	520	530	540	550
190	200	210	220	230	240	250
ACCGATGGATCCATGACGATGATTTCTCCAGAGAGTGTGTAGATTTAGATGATGATGATGATGATGATGAT						
260	270	280	290	300	310	320
CTTTTCAGGTTTGGCGATAGATATCGGGGTACAGACGGTATTCGACATCTCTCGACACAGCTTGATGA						
330	340	350	360	370	380	390
AGCCAGATCGTCTTCTCTGAC---GAAGTTATCGGTGTGGAATAT-CAGTA---GATCCGCTTCTTCTGTG						
400	410	420	430	440	450	460
ATAATGACCTCGACTCCGGTGTACAACTCTGTTGGAGAGATGTTGGCTTCTGTGTA---CACCTCTCT						
470	480	490	500	510	520	530
CTGAATCTGACGATCCGAAACAAATACGTTGAGTCAACAAATGATAGTATAGTATCCGGGTATACCTGAAA						
780	790	800	810	820	830	840
470	480	490	500	510	520	530
GCTGGTGAAGTTC---AAGAAAGTGGAGTTCCTGGGTAGTGAGTCTGCGGTAC-----GCACAAAGTTCAG						
540	550	560	570	580	590	600
CAACTAGTACGTTTGT-TGTACAGCAGGATGATTAACCCAGAGTCTTCCAGGATGATGGGTCAAGGCTCGT						
610	620	630	640	650	660	670
CATCAAGAAATACGCGTCTGGTAAACAGGACAAATATCGTTCGCAACAAATGATGCTGTGTATACATCAATGTGT						
920	930	940	950	960	970	980
600	610	620	630	640	650	660
-----CGGAGTACAAGGTCCTGATCTCGGTCTTACCCAACTGATGATGATGATGATGATGATGATGATGATG						

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90 100 110 120 130 140 150
YNGRQNFSEFWRIKPKYKVNKNNEYFIIDCIRNNSGKWSISLNKNIWTLODQAGNOKLVEYNTOM
YNSMYEFSEFWRIKPKYKVNKNNEYFIIDCIRNNSGKWSISLNKNIWTLODQAGNOKLVEYNTOM
60 70 80 90 100 110 120
ISIDYINKWIFVTITNRLNLSRIYINGNLIDEKISNLGDIHVSNDILFKIVGNDT-RVVGIRYKVFED
160 170 180 190 200 210 220
INISDYINRWIFVTITNRLNLSRIYINGNLIDEKISNLGDIHVSNDILFKIVGNDT-RVVGIRYKVFED
130 140 150 160 170 180 190
TELKTELETYSDEPSPILKDFWGNLYLNKRYLLNRLTRDKSITONS---NFLNINQORGVYKPNRI
230 240 250 260 270 280 290
KELMEKEIKDLYNQNSGILKDFWGNLYLNKRYLLNRLTRDKSITONS---NFLNINQORGVYKPNRI
200 210 220 230 240 250 260
PSNRLTYGVEVIRKNGSDTISNTONFVRKNDLAINVVDREVRLYADISIAKPEKIKLIRTSNNS
300 310 320 330 340 350 360
YLSNLYRGTKFIILKKYAS---GNKONIVNRDRVYINVVKNKEYRLATNASQAGVEKILSALEIPDVGNL
270 280 290 300 310 320 330
LGQIIVM----DSICNCTNFFQNNCGNIGLIGFHS---NNLVASSWYNNIRKNTSSNCCFWSFISKEH
370 380 390 400 410 420
SQVVMKSKNDQGITNCKNKNQNGNDIGFHFQFNNAKLIVASNNYNNQIERSRTLGCSWFEIPVDD
340 350 360 370 380 390 400
430 X
GWOEN
GGERPL
410 X

280 290 300 310 320 330 340
RTSNNSNLCOIIVMD-----SIGNCTNFFQNNCGNIGLIGFHS---NNLVASSWYNNIR
360 370 380 390 400 410
PISDSDEFYNTIQIKEYDEOPTYSCQLLFKKDEESTDEISLIGIHRFVESGIVFEYKDYFCISKWYLKEVK
350 360 370 380 390 400 410
KN--TSSNGCFWFSFISKEHGWQEN
420 430
RKPNYKLGCNWQFIPRDEGWE
420 430 X

US-09-910-186A-16 (1-432)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 164 Optimized Score = 256 Significance = -0.72
Misidue Identity = 33% Matches = 156 Mismatches = 226
Gaps = 28 Conservative Substitutions = 33

10 X 20 30 40 50 60 70
MSYNDKILILYFNKLYKIDNSIILDMRYENKFKDISGYGNSISGNDVYIYSTNRNQGIYSSKPKSEVN
FNKYNSEILNLIILNRYKNDNLIDLSGYGAKVEYDGVEL--NDKNQFKLTSSANSKIR
X 10 20 30 40 50
80 90 100 110 120 130 140
IAQNNDIYNGRYQNFSEFWRIKPKYKVNKNNEYFIIDCIRNNSGKWSISLNKNIWTLODQAGN
VTQNTIFNSVFLDSFVSFWIRPKYKNDGIGNYTHNEYTTINCMK--NNSGKWSISIRGNRIIWLIDINK
60 70 80 90 100 110 120
150 160 170 180 190 200 210
NOKLVFNMTOMISDYINKWIFVTITNRLNLSRIYINGNLIDEKISNLGDIHVSNDILFKIVGND-TR
TKSVFFYNTREDISEYINERFWFTITNN-LNNAKIYINGKLESNTDIDKIREVIANGANGIIFKLDGDDRTQ
130 140 150 160 170 180 190 200
220 230 240 250 260 270 280
YVGIRYKVFEDTELKTELETYSDEPSPILKDFWGNLYLNKRYLLNRLTRDKSITONSNF-LNINQOR
FIWMKYFSIFNTELSQNSNIERYKIQSYSLKDFWGNPLMYFNAGNKNYSYKLRKSDSPVGEILTR
210 220 230 240 250 260 270
290 300 310 320 330 340 350
GVYOKPNIFSNRLTYGVEVIRKNGSDTISNTONFVRKNDLAINVVDREVRLYADISIAKPEKIKLI
SKYNQNSKILNYRDLTYGGERFIRKNSOSINDIVRKEDYIYLDFFNLNOEWRVYTYKFKKEEKLFLA

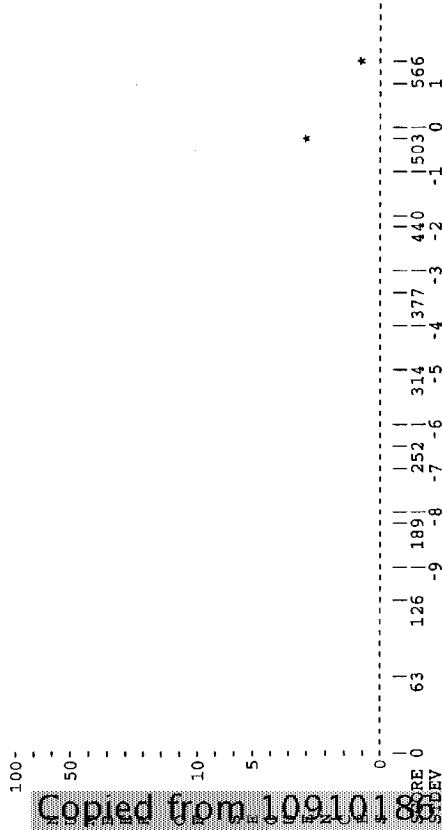
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-17.res made by bobryen on Thu 7 Nov 102 14:45:51-PST.

Query sequence being compared: US-09-910-186A-17 (1-1368)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-17 (1-1368) with:
File: US08123975A.seq



PARAMETERS

Similarity matrix Unitary K-tuple 4
Match penalty 1 Joining penalty 30
Gap penalty 5.00 Window size 500
Size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Mean Median Standard Deviation
520 499 39.26
CPU 00:00:00.00
Total Elapsed 00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig. Frame
1. US-08-123-975A-6	Sequence 6, Application U 1351	566	797	1.17	0
2. US-08-123-975A-4	Sequence 4, Application U 1338	498	706	-0.56	0
3. US-08-123-975A-1	Sequence 1, Application U 1338	498	706	-0.56	0

1. US-09-910-186A-17 (1-1368)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 566 Optimized Score = 797 Significance = 1.17
Residue identity = 61% Matches = 829 Mismatches = 488
Gaps = 39 Conservative Substitutions = 0

TGAAGGACACCATCTGATCCAGGCTTTCACAACTACATCTCCCAACCGCATCTGTCGCC
ATGGCTTTCACAACTACATCTCCCAACCGCATCTGTCGCC
X 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000

X	10	20	30	40	50	60	70
Y	10	20	30	40	50	60	70

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```
|||||
GCTCTGG-----AAATCCGACGTTGGTAACTCTGCTCAGGTAGTTGTAATGAATCCAGAAGACACAGG
1060 1070 1080 1090 1100 1110 1120
1140 1150 1160 1170 1180 1190 1200
GACCACCTAGAACTGTCAGATCTGTCGAGAGAGACACCAAGACCTTCGGACTGTTCCGGTATCGGTAAAGTT
|||||
TATCAGTACAAATGCAAAA---TGAATCTGCAGGACAAACAA-----TGGTAACGATA-----
1130 1140 1150 1160 1170
1210 1220 1230 1240 1250 1260 1270 1280
CGTCAAGGACTACGTTACGTTGCGGACACCTACGACACTACTTCTGTATCTCCAGTGGTACCTGCGTGG
|||||
--TCGTTTCATCGGTTTCACAGTTCACAAATATCGCTAAACTGGTGTGCTTCCAACTGGTACAACTCGTCA
1180 1190 1200 1210 1220 1230 1240
1290 1300 1310 1320 1330 1340 1350
TATCTCCGAGAACATCAACAAGCTGGGCTGCGGATGTAACCTGGCAGTTTCATCCAGTCGACGAGGTTGGAC
|||||
GATC-----CAAGGT-TCCTCTCGCACTCTGGGTGCTCTGCGGAGTTCACTCCCGGTTGATGACGGTTGGGG
1250 1260 1270 1280 1290 1300
1360 X
CGAGTAATAGGAATTC
|||
TGAACGTCGCGCTGTGTAAACCGGGAAGCTT
1310 1320 X 1330
```



```
GG--TTACATGTACCTGAAGGTCGGTCTGTTCTGTTATGACTACACACATCTACCTGAACCTCTTCCCTGT
830      840      850      860      870      880      890
AGTCGGAGATGTTCTGCTTCTGCTGAGTACGAGATGAGATGGAC-TTGGCGTTGAGCTGATCAGG
900      910      920      930      940      950      960
ACCGTGTACCAATTCATCATCAAGAAATACCGTCTGTACAGAGGACAAATATCGTTCGCAACAATGATC
970      980      990      1000      1010      1020      1030
GTCCAGATGATACGGTTTCCTTCTGATGGAGACCTCCAAACCGAGTCTCTTGTATACAGAGATCATGGTG
1040      1050      1060      1070      1080      1090      1100
TACTCGTCTGCGAGTAGGCTCGATGTCGTTGTTGTTT-GTACTTTGGGGTACGGACCCAGAGTTGATGGA
1110      1120      1130      1140      1150      1160      1170
GAACTTTCGAACATGAGTCGTAGAGGA---CGAACTTGGACTGGTGGCGGTGATGTTGAGTCTCGGA
1180      1190      1200      1210      1220      1230      1240
TTTCATCGTTTCAC--CAGTCAACAATATCGTAAACTGTTG-----CTTCCAACTGTACA
1250      1260      1270      1280      1290      1300      1310
GTAACCGGAGGTCGATCAGACACACACACAGTAGGAC-AGGGACAGATGGCGTTCGAGAGATGTTG
1320      1330      1340      1350      1360
AGATGTAGTGTGTAAGACCTGATCAGGATGGTCTTCATCGTGAATT
1370      1380      1390      1400      1410      1420      1430
GGTGAACGTCGCTGTAAACCGGGAAGCTT
1440      1450      1460      1470      1480      1490      1500
US-09-910-186A-17' (1-1368)
US-08-123-975A-6 Sequence 6, Application US/08123975A
Partial Score = 24 Optimized Score = 52 Significance = -1.15
Residue Identity = 42% Matches = 68 Mismatches = 81
Gaps = 10 Conservative Substitutions = 0
X 10 20 30 40 50
GAATTCCTATTAATCTCGTCCCAACCTCTGCTGACTGGGATGAACTGCCAGTTA
1190      1200      1210      1220      1230      1240      1250
1190      1200      1210      1220      1230      1240      1250
CATCCAGACGACCTGTTGTTGTTCTCGAGATACGACGAGTAGTACCCTGGGAGATACAGAAAGTAGTTG
1260      1270      1280      1290      1300      1310      1320
AACGCAACCGTACAACTGAA---ACTGGGTTGCAATTGGCAGTT--CATCCGAAAGACCAAGGTTG--G
1260      1270      1280      1290      1300      1310      1320
1330      1340      1350      1360      1370      1380      1390
TCGTAGGTGTCACGAGTAACTGATCTCTGAGATACGACGAGTACCTGACCACTACCGATACCGAACA
1400      1410      1420      1430      1440      1450      1460
ACCGAATAGTAACTCTAGAGTCG-AGGCTTCGAG
1470      1480      1490      1500      1510      1520      1530
```

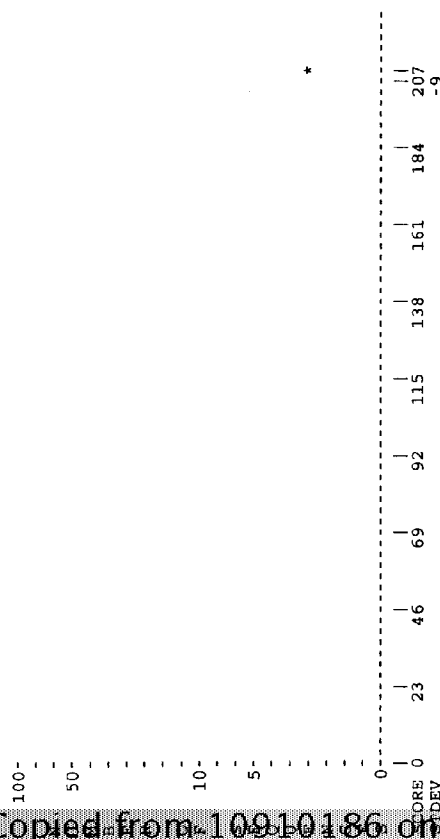

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-18.res made by bobryen on Thu 7 Nov 102 14:35:06-PST.

Query sequence being compared: US-09-910-186a-18 (1-449)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186a-18 (1-449) with:
File : US08123975A.pep



PARAMETERS

Similarity matrix PAM-150
Threshold level of sim. 16%
Mismatch penalty 1
Gap penalty 5.00
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 206 Median 207 Standard Deviation 0.58
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig. Frame
1. US-08-123-975A-5	Sequence 5, Application U	439	319	1.73	0
2. US-08-123-975A-2	Sequence 2, Application U	850	326	1.73	0
3. US-08-123-975A-3	Sequence 3, Application U	415	206	0.00	0

1. US-09-910-186A-18 (1-449)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 207 Optimized Score = 319 Significance = 1.73
Residue Identity = 49% Matches = 220 Mismatches = 182
Gaps = 9 Conservative Substitutions = 33

```

10      20      30      40      50      60      70
MKDTILQVFNNTISNTSSNAILSLSYRGRLIDSSGYGATMNVGSDVIFNDIGNGQFKLNSENSTAHQ
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
FNKNSEILNLIILNLRKDKNNLIDLSGYAKVEYDGVDELND--KNQFKLTSSANSKIRVTQ
X      10      20      30      40      50      60

```

```

80      90      100     110     120     130     140
SKFYVDSMFDNFSINFVTPPKYNNNDIQTYLQNEFTIISCIKNDGKWKVSIKGRITWTIDVNAKSKI
::: | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
NQNIIFNSVFLDFSVSFWIRPKYKNDGIONYIHNEYTIINCMKNNSGKISIRGNRIITWLTIDINGTKSV
70      80      90     100     110     120     130

```

```

150     160     170     180     190     200     210
FFEYSIKDNISDYINKWFSITINDRLGNANIYVINGSLKSEKILNLDRLINSSNDIDFKLINCTDTKFWI
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
FFEYNIREDISEYINRFFVTITNN--LNNAKIYINGKLESNTDIDKIDREVIANGEIIFIKLDGIDIDRTQIWM
140     150     160     170     180     190     200

```

```

220     230     240     250     260     270     280
KDFIFGRELNATVSSLYWQSTNTLKDFWGNPLRYDQYVLFNOGMONTIYKYFKSKMGETAPRTNEN
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
KYFSIFWTELQSQNIIEZYKIDSYSEYKDFWGNPLMYNKEYYMFNAGNKNYSIKLKSDSPVGEILLTRSKYN
210     220     230     240     250     260     270

```

```

290     300     310     320     330     340     350
NAA--INYNLYGLRFIIRKASNRNINNDNIVREGDYIYLNIDNISDESYRVYVYVNSKIQLEFLAPI
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QNSXVINYRDLYICEKFIIRKNSQSI--NDDIVRKEDYIYLDFFENLQOE--WRVYTYKYFKKEEKLFLAPI
280     290     300     310     320     330     340

```

```

360     370     380     390     400     410     420
NDPPTFYDVLYQIKKYKTYTTCQILCEKDTKTFGLFGKGVKDY--GYVWDYDNYFCISOWYLRRISEN
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
SDSDEFYNTIQIKEYDQPTYSCQLLPKDEESTDEIGLIGIHRFYESGIVFEYKDYFCISKWYLKEVKKR
350     360     370     380     390     400     410

```

```

430     440
INKLRGNCNWQFIPVDEGWTE
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
PYNLKGCNWQFIPKDEGWTE
420     430

```

2. US-09-910-186A-18 (1-449)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score = 207 Optimized Score = 326 Significance = 1.73
Residue Identity = 49% Matches = 225 Mismatches = 186
Gaps = 9 Conservative Substitutions = 33

```

X      10      20      30      40      50
MKDTILQVFNNTISNTSSNAILSLSYRGRLIDSSGYGATMNVGSDVIFND
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
EKSXVKNYKLTIMPFDLSIYTNIDILJEMFNKYNINNIILNLRKDKNNLIDLSGYAKVEYDGVDELND
390     400     410     420     430     440

```

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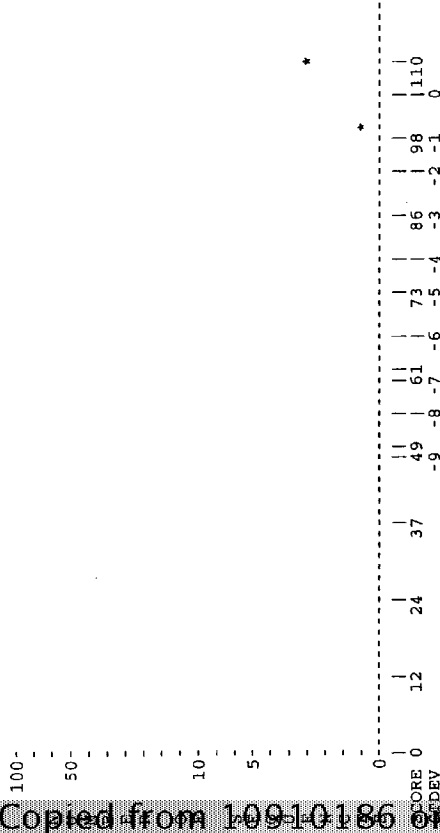
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-19.res made by bobryen on Thu 7 Nov 102 14:46:34-PST.

Query sequence being compared: US-09-910-186A-19 (1-1242)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-19 (1-1242) with:
File: US08123975A.seq



PARAMETERS

Unitary 1
Joining penalty 30
Window size 500
Gap penalty 5.00
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Mean 106
Median 100
Standard Deviation 6.35

CPU 00:00:00.00
Total Elapsed 00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.
1. US-08-123-975A-4	Sequence 4, Application U	1338	110	448 0.63 0
2. US-08-123-975A-1	Sequence 1, Application U	1338	110	448 0.63 0
3. US-08-123-975A-6	Sequence 6, Application U	1351	99	477 -1.10 0
1. US-09-910-186A-19	(1-1242)			
US-08-123-975A-4	Sequence 4, Application US/08123975A			
Initial Score	= 110	Optimized Score	= 448	Significance = 0.63
Residue Identity	= 43%	Matches	= 580	Mismatches = 0
Gaps	= 133	Conservative Substitutions	= 150	
X 10 20 30 40 50				
ATGGCTCTGAA--CGACCTGTGCATCAAAAGTTAAACAACTGGGACCTGTCTT				
CCTGATCGACCTGTCTCGTACGCTTCCAAAATCAACATCGGTTCTAAAGTT---AACTTCGATCCGATCGA				
100	110	X 120	130	140 150 160
CTCCCCGCTCTGAGACAACTTCACTACGACCTGACAAAGCGGAGAAATCACTCCGACACTAAGAT---				
170	180	190	200	210 220 230
CAAGATCAGATCCAGCTGTCTCAATCTGGAATCTTCCAAAATCGAAGTTATCTCTGAAGAACTCTCTGTATA				
170	180	190	200	210 220 230
CGAAGCTGCTGAGAAACATCTC-----TCTGGA-CCTGATCCAGCAGTACTACCTGACTTTCAACTT				
130	140	150	160	170 180
CAACTCTATGTAGAAACTTCTCCACCTCCTTCTGGAATCCGATCCGAAATCACTTCACTCCGATCTCT				
240	250	260	270	280 290 300
CGAAGCTGCTGAGAAACATCTC-----TCTGGA-CCTGATCCAGCAGTACTACCTGACTTTCAACTT				
190	200	210	220	230 240
GAACAATGATACACCATCATCACTGATGCGAAGAAATCTCTGTTGGAAGTATCTCTGAACTACGGTGA				
310	320	330	340	350 360 370
ACTGATCCGACATCAAGCTTCCGAGACGCAAGAAATACGAACTGGACAAATA-----CAC				
250	260	270	280	290 300
AATCATCTGGACTCTGCAGGACACTCAGGAAATCAACACGCTGTTGTTATTCAAATCTCTCAGATGATCAA				
380	390	400	410	420 430 440 450
CATGTTCCACTACCT-----GCGTCTCAGGAATTCGACACGGTAAATC-TCGATACCTCTGACTACTC				
310	320	330	340	350 360 370
CATCTCTGACTACATCAATCGTGGATCTTCGTTACCATCACCAACATCGTCTGAACTCCAAATCTA				
460	470	480	490	500 510 520
CGTTAACGAGCTCTGTAACCGCTCTCGGTTAC-----ACCTCTCTCTCTCCGACTAC-----				
380	390	400	410	420
CATCAACGCGCTCTGATCGACCAAGAACCGATCTCCAAATCTGGGTAAATCCACGCTCTTAATACATCAT				
530	540	550	560	570 580 590
-----GTTAAGAAAGTTAAACAAAGCTACTGAAGCTGATGTTCTCTGGTTGG--GTTGA				
430	440	450	460	470 480
GTTCAACTGACCGTTGCTGACACTACCGCTACATCTGGATCAATATCTCTCAATCTGTTGTCGACAAAGA				
600	610	620	630	640 650 660
ACAGCTGTTTACGACTCAACGAC-----GAAACTTCTGAAGTTCCACCACTGACAAATCTGCTGACA				
490	500	510	520	530 540
ACTGTAACGAAAGAAATCAAGACCTGTAGACACACCGTCCAAATCTCTGTTATCTGTAAGACTTCTGGG				
670	680	690	700	710 720 730
TCATCTATCATCATCCGCTACATCCGCGCGCTCTGAAATCGGTAAATCTCTGTAAGACGAGCTCTGTT				
550	560	570	580	590 600 610

Final Score	=	99	Optimized Score	=	477	Significance	=	-1.10
Sequence Identity	=	44%	Matches	=	582	Mismatches	=	626
Gaps	=	113	Conservative Substitutions	=	0		=	0

Copied from 10910186 on 05-05-2004

TGCAATTGGCAGTTTCATCCCGAAAGACGAAAGGTTGGACCCGAATAGTAACCTCTAGAGTCGAGGCC
1290 1300 1310 1320 1330 1340

Copied from 10910186 on 05-05-2004

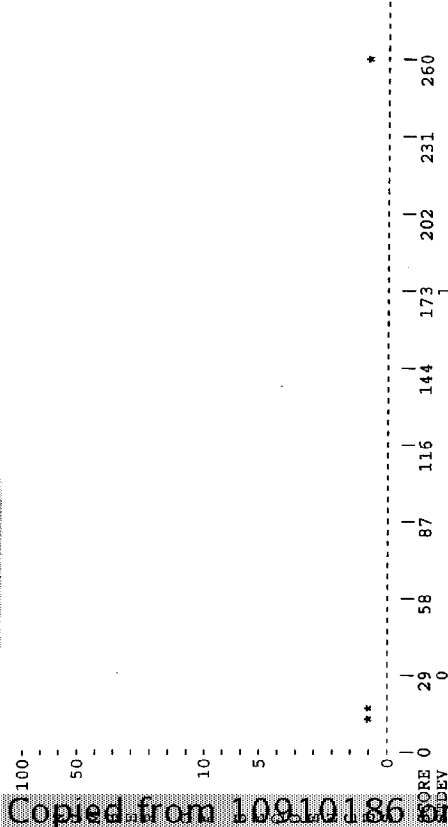
> O <
> O <
> O <

PastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-20.res made by bobryen on Thu 7 Nov 102 14:35:30-PST.

Query sequence being compared: US-09-910-186A-20 (1-413)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-20 (1-413) with:
File : US08123975A.pep



PARAMETERS

Similarity matrix PAM-150
Threshold level of sim. 16%
K-tuple 1
Joining penalty 20
Window size 413
Gap size penalty 1
Gap size 5.00
Gap offset score 0.05
Randomization group 0

SEARCH STATISTICS

Mean 97
Median 17
Standard Deviation 140.59
Total Elapsed 00:00:00.00

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Score Init. Opt.

1. US-08-123-975A-2 Sequence 2, Application US/08123975A
Residue Identity = 260 Optimized Score = 297 Significance = 1.16
Gaps = 45% Matches = 189 Mismatches = 19
Conservative Substitutions = 5
2. US-08-123-975A-3 Sequence 3, Application U 415 17 181 -0.57 0
3. US-08-123-975A-5 Sequence 5, Application U 439 16 179 -0.58 0

1. US-09-910-186A-20 (1-413)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score = 260 Optimized Score = 297 Significance = 1.16
Residue Identity = 45% Matches = 189 Mismatches = 19
Gaps = 5 Conservative Substitutions = 5

X 10 20 30 40 50 60 70
MALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEITSDTNEAAEENISLDLIQVYLTFTNEDNEPENISIE
APGICIDVDNEDLFFIADKNSFSDLSKNERIENTQSNYIENDFPINE-----LILDTDLISKIPLSE
X 10 20 30 40 50 60

80 90 100 110 120 130 140
LSSDIIGQLELMPNIEFPNGKYYELDKYTMFHYLRAQEFHGKSKRIALTNSVNEALLNPSRYTFFSSDYV
NTESLTDNFVDPVYKQPAKKIFTDENTIFQYLYSQTFPLDIRDISLTSFDDALLFSKNKYVSFFSMYI
70 80 90 100 110 120 130

150 160 170 180 190 200 210
KVKNAEAMFLGWELVDFDETSEVSTDTKDIADITIIPIYGPALNIGNMLYKDDFVGALIFSGAVI
KTANKVVEAGLFAGVYKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKNGENAFETAGASI
140 150 160 170 180 190 200

220 230 240 250 260 270 280
LLEFIEPIALVGTALVSYIANKVLTQVTDNALSKEKNEWDEVYKIVTNMLAKVNTQDLIRKKNKEA
LLEFIEPELLPVVYKQPAKKIFTDENTIFQYLYSQTFPLDIRDISLTSFDDALLFSKNKYVSFFSMYI
210 220 230 240 250 260 270 280

290 300 310 320 330 340 350
LENOAETAKAIINQYNOYTEBEKNNINENIDLSKLNESINKAMINIKFLNOCVSYLMSWIPYGVKR
LNYOQALEEIIKYRYNIYSEKESINIDFNDINSKLNESINKAMINIKFLNOCVSYLMSWIPYGVKR
290 300 310 320 330 340 350

370 380 390 400 410 X
LEDFDASLKDALLKYIRDNYGTLIGQVDRKDKVNTLSTDPFOLSXYVDNQ
LLEFIEPELLPVVYKQPAKKIFTDENTIFQYLYSQTFPLDIRDISLTSFDDALLFSKNKYVSFFSMYI
360 370 380 390 400 410 420

N

2. US-09-910-186A-20 (1-413)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score = 17 Optimized Score = 181 Significance = -0.57
Residue Identity = 9% Matches = 41 Mismatches = 342
Gaps = 5 Conservative Substitutions = 25

X 10 20 30 40 50 60
MALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEITSDTNEAAEENISLDLIQVYLTFTNEDNEPENI
RYENHLIDLSRYASKINIGSKVNFDPIDKNOQLFNLESKIEVILKNAIVNSWYENFTSWFIPIKYF
X 10 20 30 40 50 60 70

70 80 90 100 110 120 130 140
SIENLSSDIIGQLELMPNIEFPNGKYYELDKYTMFHYLRAQEFHGKSKRIALTNSVNEALLNPSRYTFFS

NSISLNNETIINCNN-----SGWKVSLNYGELIWTLODTEIKQVVFYKYSQMINSDYNRWIFVTIT
80 90 100 110 120 130
SDYVKKVKNKATEAMFLGWVEQLVYDFDTSEVSTDKIADITIIPIYIGPALNIGNMLYKDDFVGALIFS
150 160 170 180 190 200 210
NNRLNNSKIYINGRLIDQKPSINLGNHASNINMFKLDGCRDTHRYIWKYENLFDKELNEKEIKLDYDNOS
140 150 160 170 180 190 200 210
GAVILLEPPIPIALVIGTALVSYIANKVLTQTDNALSKRNEKDEYKIVTNWLAKVNTQIDLRKK
220 230 240 250 260 270 280
NSGILKDFWGDYLDKPYMLNIDYDNKYVDVNNVIGIRGYMYLKGPRGSVMTNIIYLSLSYRGTKFLIKK
220 230 240 250 260 270 280
MKEALENGAEATKALINQVQNYQTEEEKNNINIDDLSSKLNESINAKMININKPLNOCVSYLMSWIPY
290 300 310 320 330 340 350
YASGNKONIVANNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVYVNMKSKNDQGITNKCK
290 300 310 320 330 340 350
GVKRLDFDASLKDALLKYTRDNYGTIGQVDRKDKVNNLTSTDIPQLSKYVDNQ
360 370 380 390 400 410 X
MNLQDNNCNDIGFIFGHFNNAKLVASNNYNNQIERSSTLGCSSWEFIPVDDGNGERPL
360 370 380 390 400 410 X

US-09-910-186A-20 (1-413)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Optimal Score = 16 Optimized Score = 179 Significance = -0.58
Residue Identity = 11% Matches = 47 Mismatches = 340
Conservative Substitutions = 20

10 20 30 40 50 60 70
MALNDLCIKVNNDLFPSPEDNFTNDLNGEITSDTNIERAAENISLDLIQYVLTENFNEPENISIE
FNKYNSEIILNLIILNRYKNNLIDLSGYGAKVEYDQVDELNDKXNQFLASSANSKIRVTONON
X 10 20 30 40 50 60
80 90 100 110 120 130 140
LSSDIIGOLELMPNIEFPNGKYELDKYTMFLRAQEFHGKSRIALTNSVNEAL----LNPSRVYTF
IIFNSVFLDFSVSWIRIPKYKNDGIGNYIHNEYTIINCMMKNSGKKISIRGNRIIWTLLIDINGTKSYFFE
70 80 90 100 110 120 130
150 160 170 180 190 200 210
SDYVKKVKNKATEAMFLGWVEQLVYDFDTSEVSTDKIADITIIPIYIGPALNIGNMLYKDDFVGALIFS
YNIREDISEYINRWFFVTIINLNNAKIYINGKLESNTDKIDREVIANGELIEFKLDGIDRTOPIWKKYFS
140 150 160 170 180 190 200

GAVILLE-----FPEIAPVIGTALVSYIANKVLTQTDNALSKRNEKDEYKIVTNWLAKVNTQ
IFNTELSQSNIEERYKIQSYSEYKDFWGNPLMYNKEYYMFNAGNKNYSYIKLKDSPVGEILTRSKYNQNSK
210 220 230 240 250 260 270 280
280 290 300 310 320 330 340
IDLIRK-----MKKEALENGAEATKALINQVQNYQTEEEKNNINIDDLSSKLNESINAKMININFP
YINTRDYIGEKEKIIIRKKSNSQSINDDIVRKEDYIYLDFFNLNQEMRVYTYKYFKKEEKEKFLAPISDSDEF
290 300 310 320 330 340 350
350 360 370 380 390 400 410
INQCSVSYLANSMPGVKREDFDASLKDALLKYTRDNYGTIGQVDRKDKVNNLTSTDIPQLSKYVDN
YNTIQIKEYDEQTYSCQLLFKDESDTEIGLIGHRFYESGIVFEETKDYFCISKWYLKEVKKRPNLKL
360 370 380 390 400 410 420

X

Q
GCNNQFIPKDEGWTE
X 430


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ACACCGACCTACTCTTCCGAGCTGCTGTTTCAGAGAAAGTAAAGATCTACTGACGAAATCGGTGTATCGG
1100      1110      1120      1130      1140      1150      1160      1170
AGTCGTCGGTCCCTCTCTGTTGGAGTCTCTACATCGACAAAGAAATCATCAAGACCATCGACACGCG
670      680      690      700      710      720      730
TATCCACCGTTCTTACGAATCTGCTATCGTATTCGAGATACAAAGACTACTCTCTGCATCTCCAAATGGTA
1170      1180      1190      1200      1210      1220      1230
740      750      760      770      780      790      800
TTTGACCAAGAGAACAGAGAGTGGTCCGACATGTAGGTTTGTATCGTCGCCCAATGGTGTGTCACCGCTCAA
1110      1120      1130      1140      1150      1160      1170
CCTGAAGAGAGTCTTAAACGCAACCGTACACCTGAA-----ACTGGTTGCAATGGCAGTTCTATCCGGAA
1240      1250      1260      1270      1280      1290      1300
810      820      830      840      850      860      870
CACCCAATCTACACCAATCAAGAGGAGTATGTA--CAAGCGCTTGACTACAGGCGCCCAAGCTTTGG
1310      1320      1330      1340      1350
AGACGAAGGTTGGACCGAATAGTAACTCTAGAGTCGAGCGCTGCAG
1310      1320      1330      1340      1350

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US-09-910-186A-21 (1-1242)

US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 88 Optimized Score = 394 Significance = -0.54
 Residue Identity = 41% Matches = 459 Mismatches = 582
 Gaps = 77 Conservative Substitutions = 0

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140      150      160      170      180      190      200
TTCCCAATCAAGAGTTGATTTGGACACCGACTTGTATCTCCAGAGTCCAGTGGCATCCGAGACACCGGAG
210      220      230      240      250      260      270
TCCTTGACTGACTTCAAGTCGAGCTCCCGAGTCTAGAGAGAACACAGCTATCAAGAGATTTTCAACGAC
RACATCAATCAATCTCCATCTCCAGCTCCGAGTACGATCCCAATCACTGATCCAGCTGCTCGGTACGCT
50      60      70      80      90      100      110
GAGAACACATCTTCCCAAT-ACCCTGACTCTCAGACCTTCCCTTTGGACATCAGACATCTCCCT-----TG
280      290      300      310      320      330      340
TCCAAATCAACATCGGTCTTAAAGTTAACTTCGATCCGATCCGACACAGATCAGATCCAGCTGTTCAATCTG
120      130      140      150      160      170      180      190
350      360      370      380      390      400      410
ACCTTTCTTCGAGAGCGCCCTGCTTCTCCAAAGAGTCTACTCTTCTTCCATGAGTACATCAAG
GAATCTTCCAAATCGAAGTTATCCTG-----AAGAAATGCTATCGTATACAACTCTATGTAC-----
200      210      220      230      240
420      430      440      450      460      470      480
ACTGTAACAAGGTCGTCGAGCGCGTGTTCGCTGGTGGTCAAGCAGATCGTCAACGATTTGCTGATC
-----GAAACCTTCCACCTCTCTCGACCTGATCCGAAATCTTCAACTCCATCTCTCTGAAACAT
250      260      270      280      290      300      310
490      500      510      520      530      540      550
GAGGCTACAGTCCACACCATCGAGCAAGATTCGCG-----ACAATCTCTTGAATGTGCCATACATCGGT
560      570      580      590      600      610      620
TTGSCCTTGAACGTCGTTAGACAGACCGCCCAAGGTAACCTTCGAGACAGCTTTCGAGATCGGTGGCTCC
TGGACTCTGAGGACACTCAGGAATCAACACAGCTGTTGTTATTCAAATCTCTAGAT-----GATCAAC
390      400      410      420      430      440      450
630      640      650      660      670      680      690

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ATCTTGTGGAGTTCATCCACAGAGTGTTCATCCAGTCTGTCGGTGCCTCTTGTGGAGTCTCTACATCGAC
1111      1111      1111      1111      1111      1111      1111
ATCTCTGACTACATCATCTGATCTGATCTGTTTACCATCACCACAAATGCTGTGATAACTCCAAATCTAC
460      470      480      490      500      510      520
700      710      720      730      740      750
AACAGAAC---AAGATCATCAAGNCCATCGAACGCTTTGACCAGAGAAACG-----AGAAGTGG
1111      1111      1111      1111      1111      1111
ATCAACGCGCTGTGATCGACCGACCAACCGATCTCCAATCTGGTAAACATCCACGCTTCTAATAATCATG
530      540      550      560      570      580      590
760      770      780      790      800      810      820      830
TCCGACATGTACGGTTTGTGCTGCGCCCAATGTTGCCACGTC--AACACCCAAATCTACACCATCAAGGA
1111      1111      1111      1111      1111      1111
TTCAACTGTACCGTTTCTGTCGACATCCACCGCTATCTGGAATCAATCTCTCAATCTGTTTCGCAAGAA
600      610      620      630      640      650      660
GGGTATGTACAAGSCCTTGAA-----CTACAGGCGCCCAAGCTTTGGAGGAGATCATCAAGTACAGATCAAC
840      850      860      870      880      890
CTGAACGAAAGAAATCAAGACCTGTACGACACACCGTCCAAATCTCTGATCTCTGAAAGACTTCTGGGT
670      680      690      700      710      720      730      740
900      910      920      930      940      950      960
AATCTCTCCGAGAGGAGAGTCCAAATTAACATCGACTTCAACGACATCAACTCCAGCTGGAACGAGGT
1111      1111      1111      1111      1111      1111
GACTTACCTGTCAGTACGACAAACCGTACTACATCTGAATCTGTACGATCCGAAACAAATACGTTGACG-----
750      760      770      780      790      800      810
970      980      990      1000      1010      1020      1030      1040
ATTAACAGGCCCATCGACACATCAACACACTTCAATCAAGGTTGTCCTCTCTACTGTGTAAGAGATG
1111      1111      1111      1111      1111      1111
-TCAACAATGTAGTATCCCGGTTACATGATCTGAAAGGTCGCGGTGTTCTGTATGACTACCAACAT-
810      820      830      840      850      860      870
1050      1060      1070      1080      1090      1100      1110
ATTCATGTGCGCTCGAGAGATGTTGGACTTCGACACACCTGAGAGACTGTTGACTACTACGAC
1111      1111      1111      1111      1111      1111
CTACTCTCAATCTTCCCTGTACCGTGTAC--CAATTCATCATCAAGAAATACCGCTCTGTAACAAGGAC
880      890      900      910      920      930      940
1120      1130      1140      1150      1160      1170      1180
GAGAACAGTTGTAC-TTGTATCGGTCGCTGAGTACGAGAGTCCCAAGGTCAACAAGTACTTTGAAGACCAT
1111      1111      1111      1111      1111      1111
AATATCTTCGCAACAATGATCGTGATACATCAATGTTGTAGT-TAAGAACAAAGATACCGTCTGCTAC
950      960      970      980      990      1000      1010
1190      1200      1210      1220      1230      1240      1250
CATGCCATTCGACTTGTCCATCTACACCAACGACACCATCTTGTATCGAGATGTTCTAA
1111      1111      1111      1111      1111      1111
CA-----ATGCTTCTCAGGCTGGGTAGAAAAGATCTTGTCTCTGGAATCCCGGACGTTGGTAATCTGT
1020      1030      1040      1050      1060      1070      1080
CTCAGG
1090

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3. US-09-910-186A-21 (1-1242)

US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 88 Optimized Score = 394 Significance = -0.54
 Residue Identity = 41% Matches = 459 Mismatches = 582
 Gaps = 77 Conservative Substitutions = 0

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TTCCCAATCAAGAGTGTGATCTTGGACACCGACTTGTATCTCCAAAGATCGAGTTCGATCCGAGAACACCGGAG
140      150      160      170      180      190      200
CTCGGCCATGGCTCG--TCTGCTCTCTACCTTC--ACTGAATACATCAAG
X      10      20      30      40
210      220      230      240      250      260      270
TCCCTGACTGACTTCAACGTCGACGCTCCAGTCTACGAGAACCAACAGCTATCAAGAAGATTTTCACCGAC
1111      1111      1111      1111      1111      1111

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640      670      680      690      700      710      720
CGTTCTCGAAGTTACCTTGGCGGTCTCGTTACCGAGTTCAGAGGCCAACCG-ATGTATGGGACAATCAAG
|||||
ACTTCTGGGTGACTACCTCGAGTACGACAAACCGTACTACATGCTGTAATCTGTAGATCCGACAAATACG
730      740      750      760      770      780      790      800
710      720      730      740      750      760      770
GAGATGTCGGCAATCT---TGTCAGGT---GTGGAGTGTGTAGCTCGATGAGAAATCGTTGACGATCT
|||||
TTGAGCTCAACAATGTAGTATCGCGGTCTACATGTACTGAAAGTCCGCGTGTCTGTATGACTACCA
810      820      830      840      850      860      870
780      790      800      810      820      830      840
GCTTGACCCACAGCGAACAACCGGCTTCAGG-ACCTGTGTACAGCTGTGTAGTCTAGTCCATGGAGAAG
|||||
ACAT-----CTACCTGAACTCTTCCTCGGTGGTACCAATTCATCAAGAAATACGGGTCTGTGTAAC
880      890      900      910      920      930      940
850      860      870      880      890      900
AAGGAGTAGACTCTTGGAGAACAGCAGCGCTCTCGAAGAGAGGTCAAGAGATGCTCTGATGCTC
AAGGACAATATCGTTCGCAACAATGATCGGTATACATCAATGTTGTAGTTAAGAACA-----AAGNATACCG
950      960      970      980      990      1000
920      930      940      950      960      970      980      990
AAAGGAAAGGTCTGAGATACAGGTATTGGA-AGATGGTGTCTCGTCGGTGAATACTTCTGTAGTGTG
|||||
TCGTGCTACCAATGCTTCAGGTGTGTGAGTGTGAGAAAGATCTGTCTCTGGAATC-----CCGGACG
1010      1020      1030      1040      1050      1060      1070
1000      1010      1020      1030      1040      1050
TTGCTCTCTGAGTGGAGCTCGAGTGTGAAGTCAAGTCAAGGCTCGGTGTC---TCGGATGGCAACT
|||||
TTGGTAATCTGCTCAGGTAGTGA--ATGAAATCAAGAACAGCAGGATCACTAACAAATGCAAAAT
1080      1090      1100      1110      1120      1130      1140
1060      1070      1080      1090      1100      1110      1120      1130
CGATCTGGAGATCAAGTCGGTGTCCAAAGTCAACTCGTTGATGGGAATCGTTCGAGTGTGACT
|||||
GAATCTGAGGACAACAATGTAGTATCGGTTCATCGGTTCACCGAGTTCACAAATATCGTAAAT
1150      1160      1170      1180      1190      1200      1210      1220
1140      1150      1160      1170      1180      1190      1200
GGGTG--TTGATCTCATCTCTGCTTGTGCAAGTGTGCGGAGAGAGTCTTCTGACGATGAAGAC
|||||
GGTGTCTCAACTGTCAATCTGTCAGATCGAAGCGTTCCTCTCACA-----CTCTGGTGTCTCTTGGGAGT
1220      1230      1240      1250      1260      1270      1280
1210      1220      1230      1240      1250      1260      1270      1280
AAGTCTCTGCTCTCGAC---GTGATACAGATCTCTGGAGCCAT
|||||
TCATCCGGTGTATGACGGTGTGGGTGAACGTGCTGTAAACCGGGAAGCTT
1290      1300      1310      1320      1330
1290      1300      1310      1320      1330
CTGCTGTCTACCTTCACTGAATACATCAAGACATCAATACCTTCATCTGAACTGCGCTACGAATCC
20      30      40      50      60      70      80
X      10      20      30      40
TTAGACATCTCGATCAAGATGGTGTGTTGGTGTAGATG---GACAAGTCTG
|||||
CTGCTGTCTACCTTCACTGAATACATCAAGACATCAATACCTTCATCTGAACTGCGCTACGAATCC
20      30      40      50      60      70      80
50      60      70      80      90      100      110
AATGGCATAGG---TCTTCAAGTACTTGTGACCTTGGACTTCTGTAATCTGACTACG-----CGGAACCGATC
|||||

```

2. US-09-910-186a-21' (1-1242)

US-08-123-975a-1 Sequence 1, Application US/08123975A

Initial Score - 65 Optimized Score - 457 Significance = 0.87
 Residue Identity = 42% Matches = 556 Mismatches = 657
 Gaps = 108 Conservative Substitutions = 0

ATCATCTCTGGACTCTGATPCGATATCAACGGTGAAGA-----CCAAAATCTGTATCTCTTCGGAATACAAACAATCGCGT
370 380 390 400 410 420
410 420 430 440 450 460 470
TATACATACCCCTCTCTGTGGTGTAGAATTTGGGTTGTGACGGTGGACAAACCAT-----TGGCGCAGCATCAAAACC
TATACATACCCCTCTCTGTGGTGTAGAATTTGGGTTGTGACGGTGGACAAACCAT-----TGGCGCAGCATCAAAACC
430 440 450 460 470 480 490
GAGACATCTCTCGAATACATCAATCGCTGGTCTCTTCGTTACCATCAACCAATACCTTGAACCAATCCTAAATC
440 450 460 470 480 490
480 490 500 510 520 530 540
GTACATGTCTGGACCACT--TCTCGTTTCTCTTGTTCAAG--CGTTGTGCATGGTCTTGATGATCTTG--TTT
490 500 510 520 530 540
TATACATCAACGGTAAATCGAATCTAATACCGACATCAAAAGACATCCGTTGAAGTTATCGTTAACGGTGAATATC
500 510 520 530 540 550 560 570
510 520 530 540 550 560 570
520 530 540 550 560 570 580 590 600 610 620 630 640
ATCTTCAAACCTGGACGGTGACATCGATCGTACCGAGTTCTACTGGATGAAATACCTTCTCCATCTTCAACAC
580 590 600 610 620 630 640
620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780
AAGATGGAGCACCAGCGATCTCGAAGCGTTCTCGAAGGTTACCTTCCGGCTCTCTTACCGAGCTTCAAG
640 650 660 670 680 690 700 710 720 730 740 750 760 770 780
720 730 740 750 760 770 780
760 770 780 790 800 810
GATGACGAAATCGTTGACGATCTG-----CTTGACCCACACAGCAAAACCCGGCTCGACGACCTTTGT
780 790 800 810
ACTGAAGAAGACCTCTCCGGTTGGTGAATCTCGACTCGTTCCAAATCAACACAGAATCTTAATATACATCAA
790 800 810 820 830 840 850
800 810 820 830 840 850
830 840 850 860 870
AGCNGCTTGATGTAGTCCATGGAGAAG-----AAGGATGAGACCT--TGTTGGAGCAACG-----AGGG
850 860 870 880 890 900 910 920
CTACCGGACCTGTACATCGGTGAAAGTTTCAATCATCGTCCGCAATCTAATCTACGTCCTCATCATGATGA
880 890 900 910 920
880 890 900 910 920 930
CGTGGT--CGAAGAAGAGGTCAAGGA-----GATGTCCT--CTGATGTCCAAAGGAAGGTCTGAGAGTA
900 910 920 930
CATCGTACGTAAAGAAGACATCATCTACCTGGACCTTCTCAACTGAATCAGTAAGTGGCGGTATACACCTA
930 940 950 960 970 980 990
950 960 970 980 990 1000 1010
0 950 960 970 980 990 1000 1010
CAGGTATTGAAGATGATGTTCTGCTGGTGAATCTCTTGATAGCTGGTGGTCTCTGTAGACTGGGAC
1000 1010 1020 1030 1040 1050 1060 1070 1080
CAAGTACTTCAAGAAAGAAGAAAGAAAGCTTTTCCTGGCTCCGATCTCTGATTCGGAGCACTCTACACAC
1020 1030 1040 1050 1060 1070 1080
1020 1030 1040 1050 1060 1070 1080
GTGACGTTGAAGTCACTGAAGACTCGGTGTTCTCGATGGCACTCGATCTTGAGATCAAGTGGTGTCT
1040 1050 1060 1070 1080
CATCCAGATCAAAAGATACGACCAACGCCGACCTTACTCTTTCGCGTGTCTGTTCAAGACATGAGAATC
1060 1070 1080 1090 1100 1110 1120 1130 1140
1080 1090 1100 1110 1120 1130 1140
CA--AGATCAACTCG--TTGATTGGGA--AGTCTGTTCTCATGTAGTCTGGATCGGTGTG-----TACTCGAT
1090 1100 1110 1120 1130
TACTGACGAATCGCTGATCGGTATCCACCGTTTCTACGAATCTGTGTATCGTATTCGTAAGAATACAAAGA
1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210
1150 1160 1170 1180 1190 1200 1210
1150 1160 1170 1180 1190 1200 1210
TCTCTCGTCTCTGGCAAGTCGTCGGAAGAGGTTCTTGTACCGATGAAGCAAGTCTCTGTTCTCGAC
1170 1180 1190 1200 1210
TACTTCTGCACTTCCAAATGTTACCTGAAGCAAGTCTAAACCGCAACCTGACAACTGAACTGGTGTGGA

1220 1230 1240 1250 1260 1270 1280
1220 1230 1240 X
GTCGATACAGATTCTCTGGGCCAT
| | | | |
TTGGCAGTTTCATCCCGAAGACGGAAGTTGGACCGAATAGTAAC
1290 1300 1310 1320 1330

[illegible]

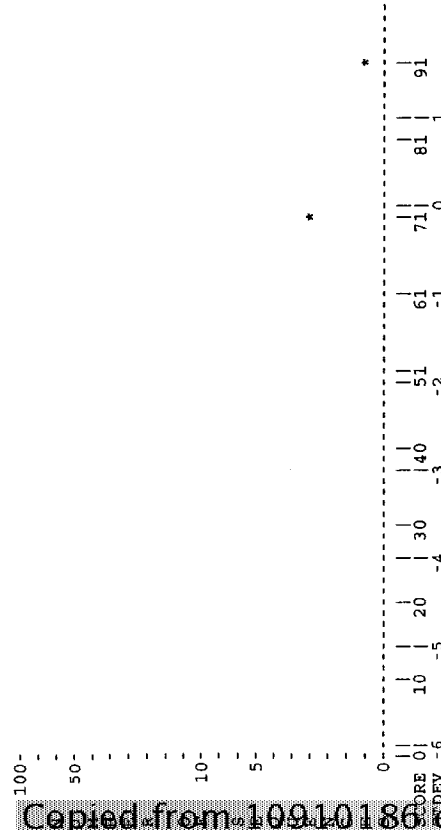
> O <
O/I/O IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-23.res made by bobryen on Thu 7 Nov 102 14:47:57-PST.

Query sequence being compared: US-09-910-186A-23 (1-1200)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-23 (1-1200) with:
File US08123975A.seq



PARAMETERS
Unitary K-tuple 4
Mismatch penalty 30
Joining penalty 500
Penalty 5.00
Window size 0.33
Gap size penalty 1
Gap score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 77 Median 72 Standard Deviation 11.55
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score above mean Init. Opt. Frame
1. US-08-123-975A-6 Sequence 6, Application US/08123975A **** 1 standard deviation 1351 406 1.21 0
2. US-08-123-975A-4 Sequence 4, Application US/08123975A **** 0 standard deviation 1338 304 -0.52 0
3. US-08-123-975A-1 Sequence 1, Application US/08123975A **** 1 standard deviation 1338 304 -0.52 0

1. US-09-910-186A-23 (1-1200)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 91 Optimized Score = 406 Significance = 1.21
Residue Identity = 42% Matches = 492 Mismatches = 571
Gaps = 100 Conservative Substitutions = 0

X 10 20 30 40 50
ATGTCCCTGTACAAAGACCCCTTGACTGTAGAGAGCTGCTGGTGAAGAACA
CTGTTTCCTTCGTGATCCCGAATACAAAGACGCGGTATCCAGAAATACATCCCAATGAATACA
230 240 250 260 270 280 290 300
CTGACCTGCCATTCATCGGTGACATCAGTCACTGAGACTGACATCTTCCTGCTAGGAGCATCAAGAGG
130 140 150 160 170 180 190
AGACTGAGGTGATCTACTACCCAGCAACGCTGTACAGCAAGTGTCTTCAGTAAGCAACCTCCGA--
CTCTGATCGATATCAAGGTAAGACCAATCTGTATCTTCGATACACATCCGTTGAGAGATCTCTGAAT
380 390 400 410 420 430 440
200 210 220 230 240 250 260
GCATGGACAACCTAGCTGCTTACC---CTAGTATCGACAGTGTAGAGTGTAGATC--CTGCCAGGGAGAA
ACATCAATCGTGTCTTCTGTTACCATCACCATACCTGTACATCTTAAATCTACATCAACGTTAAAC
450 460 470 480 490 500 510
TCAAGTCT-----TCTACGACAACCGTACCAGAACGTTGACTACCTGAACTCCTACTACTACTAG
TGAATCTAATACCGACATCAAGACATCGTGAAGTATTCGCTAAC--GGTGAATCAT-CTTCAAACTGG
520 530 540 550 560 570 580
AGTCTCAGAGCTGAGT-----GACAACGTGGAGGACTTCACCTTCACCGGTTCA-ATCGAGGAGCTCTGG
ACGGTGACATCGATCGTACCCAGTTCATCTGGATGAATATCTTCCATCTTCAACACCGAACTGTCTCAGT
590 600 610 620 630 640 650
390 400 410 420 430 440 450
ACAACAGTCAAGGTGTAC-ACTTACTTCCCTACCTGCTGTACAGGTGTATCCGCTGTGCAAGTGGT
CCATATCGAAGAACGTTACAGATCCAGTCTTACTCCGAAATACCTTGAAGACTTCTGG-----GGT
660 670 680 690 700 710
460 470 480 490 500 510 520 530
CTGTTCTCGATGTGGCAACAGGTGGTTGAGGACTTCACTACCAACATCTGCGTGAAGACACACTGGAC
AATCCGCTGTATGTACAAACAAAGATATCTATGTTCAATGCTGTGTACCAAGACTCTTACATCAAACTAAG
720 730 740 750 760 770 780
AAGATCTCAGATGTGTACATATCC-----CTACATCGGACCGGCACTGAACAT-CTCCAACT-----
AAAGACTCTCGGTGTGGTGAATCCCTGACCTCGTTCCTCAATACACCGAGACTCTAATATCATCACTACCGG
790 800 810 820 830 840 850 860
---CTGTGCTGTGGAACTTCACTGAGGCAATTCGAGTCTACTGTGTACCACTCTCTGCTGGAGGCATTC

GAACATCTCCAAACTCTGTGCGCTGCTGGAAACTTC-----ACTGAGGCATTCGCAGTCTACTTGGTGTCAACCATCC
170 180 190 200 210 230
AATCAGATCCCA--GCTGTTCATCTCGAATCTCTCAAAATCGAAGTTATCTCTGGAAGATGCTATC--GTATAC
650 660 670 680 690 700 710
TCTGGAGCATCTCCTGAGTTCACAATCCTCTGCTGGTGCAT--TGTGTATCTACAGTAAGTCCAGGAG
AATCTATG--TAGGAAACTTCTCCA--CTCTCTTCTGGATCCGATCCCGAAATACTTCAATCTCAATCTCT
240 250 260 270 280 290 300
220 730 740 750 760 770 780
CGAAACGAGATCATCAAGACCATCGCAACTGCTCTGGACGACGAGGATCAAGAGATGGAAGACTCTCTACGAG
CTGAAC----AATGATACACCATCATCAACTGCATGGA--AAACAATCTCTGTTGGAAAGTATCTCTGCACT
310 320 330 340 350 360 370
790 800 810 820 830 840 850
TGTGATGAGGGAACGTGTTCTCAGGATCATCAACCGAGTCAACA-----ACATCTCTACACAGA
ACGCTGAAATCATCTGGAGACTCTGCAGCACACTCAGGAAATCAACAGAGGCTGTGTATTTCAAACTACTCTCAGA
380 390 400 410 420 430 440
TGTTACGATCTCTGAACTACGACGCGTGCATCAAGCTTAAGATCGACTGGAGTACAGAAAGTACTCCCG
TGATCAACATCTCTCACTACATCAATCGCTGGATCTCTGTTACCATCCACAACTGCTGTGATACACTCCA
450 460 470 480 490 500 510
930 940 950 960 970 980 990
GAAGCGCAAGAGAAACATCAAGAGCCAGCTGTGAGACTCTGAAGACACTCTGGACCTCAGATCTCGGAGG
AATCTCATATCAACGGCCGCTGTATC---GACCAGAAACCGATCTCCAACTCTG---GGTACATCTCAACGCTT
520 530 540 550 560 570 580
1000 1010 1020 1030 1040 1050 1060
CAATGAACAACATCAACAAGTTCTCCGAGAGTG---CTCGGTACCTACCTGTGTGAAGACATGTGCTGCTA
CTAATAACATCATGTTTCAAACCTGGACGCGTGTCTGTGACACTCAACGCTACATCTGGATCAAAACTTCTCAATC
590 600 610 620 630 640 650
1070 1080 1090 1100 1110 1120 1130
AGGTCAATCGAGCTGAACGAGTTCAGCCAAACACCAAGCAAGTGTATCACTGTATCGACTCCCATTA
TTGTCGACAAAGAACTGAA-----CGAAAGAAAGAAATCAAAAGACCTGTACGACACACAGCTCAATCTCGTGA
660 670 680 690 700 710 720

US-09-910-186A-23 (1-1200)
US-08-123-975A-4 Sequence 4, Application US/08123975A

T C T G A A C A C T T C G G G T G A C T A C C T G C A G T A C C A C A A C C G T A C T A C A T G T G T A A T C T G T A C C A T C C G A
 730 740 750 760 770 780 790
 A C A A A T A C G T T G A
 800

ACAATACGTTGA
800

```
Initial Score = 71 Optimized Score = 304 Significance = -0.52
Residue Identity = 43% Matches = 365 Mismatches = 401
Gaps = 71 Conservative Substitutions = 0
```

CACGCGTTCAATCGAGAGGCTCTGGACACACAGTGCAGAAAGTGTCACATTACTTCCCTACCCCTGGGTAAACA
 CTCGAGCATGGCTCTCTGCTGCTCTACCTTCACTGAATCATCAAGAACAT
 x 10 20 30 40 50
 440 450 460 470 480 490 500
 GGTGAATCCCGTGTGCAAGTGTCTTCCTGATGTGGCGCAACAGCTGGTGTGAGGACTTCTCATCCAA

GGTGAATGCCGGTGTGCAGGTGGTCTGTTCTCTGATGATGGGCAACGACGGTGGTTGAGGACTTCACTACCAA

Copied from 10910186 on 05-05-2004


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TTCGACAAAGAACTGAACGAAAGAAATCAAGACCTGTACGACAAACAGTCCCAATTCCTGATCTCGAA
660 670 680 690 700 710 720

GATGTGTAGTGAAGTCCCTCAACACGTC-----GTTTGGCCCA--CATCAGGAACAGACACCTGTG
700 710 720 730 740 750
|||||
GACTTCTGGGTGACTACCTGACGACGACAAACCGTACTAGTCTGAATCTGACGATCCGAAACAAATAC
730 740 750 760 770 780 790 800
|||||
CACACCGCATTCACCTTGTAGCCAGGT---AGGAAAGTAAAGTGTACACCTTGGCACTGTTCTCCAGACG
760 770 780 790 800 810
|||||
GTGACGTCACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
810 820 830 840 850 860 870 880
|||||
CTCCCTCGA-TTGAACGGGTGAAGTCCCT-CCACGTTGTACTCAGCTCTGAGACTCTAGTAGTAG
820 830 840 850 860 870 880
|||||
AACATCTACCTGAACTTTCCTGACCGGTGACCAATTCATCATCAAGAAATACCGCTCTGTAACAAG
880 890 900 910 920 930 940
|||||
TAGGA----GTTCAAGTAGTCCAGTCTCGGTACCGTGTGTGAGAGACTGTATCTCCCTGGGAGGAT
890 900 910 920 930 940 950
|||||
GACATATCGTTCGACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
950 960 970 980 990 1000 1010
|||||
ACCAAT---GCTTCTCAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
1020 1030 1040 1050 1060 1070 1080
|||||
GATCA-CTTGGTCTACTGACA-CGTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG
1030 1040 1050 1060 1070 1080 1090
|||||
TCTCAGGTAGTGTAAATGAAATCAAGACGACGATGATGATGATGATGATGATGATGATGATGATGATG
1090 1100 1110 1120 1130 1140 1150
|||||
AGGAAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
1100 1110 1120 1130 1140 1150 1160
|||||
AGGAAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
1160 1170 1180 1190 1200 1210 1220
|||||
CTCTCTACAG--TCAAGGGTCTTGTGTACAGGACAT
1170 1180 1190
|||||
CTTCCAACTGGGTACAAATGCTCAGATGCAACGTTCTCTCTGACACTGTGGTTCCTTTG
1230 1240 1250 1260 1270 1280
|||||

US-09-910-186A-23' (1-1200)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 73 Optimized Score = 449 Significance = 0.58
Residue Identity = 42% Matches = 527 Mismatches = 653
Gaps = 62 Conservative Substitutions = 0

X 10 20 30 40 50
TTAGTCTGGAAGCTGTTGTTTACCTTTCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC
60 70 80 90 100 110 120
ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
90 100 110 120 130 140 150
AATCACCCTGAT-CGACCTGCTCTGCT-ACGCTTCCAAATCAACATCGGTCTTAAAGTTAACTTCGATCCGA
130 140 150 160 170 180 190
TCGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
160 170 180 190 200 210 220

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TTCGACAAAGAACTGAACGAAAGAAATCAAGACCTGTACGACAAACAGTCCCAATTCCTGATCTCGAA
160 170 180 190 200 210 220 230
|||||
ATGTTGTTCAATGCTCCGAGATCTTTGAGTCCAGACTGTTCTTCAAGTCTTCAACCTGGCTCTTGAITTC
200 210 220 230 240 250 260
|||||
GTATACAACTCTATGTAGCAAAATCTTCCACCTCTTCTGATCGTATCCGAAATACCTTCAACTCCATC
240 250 260 270 280 290 300
|||||
TCCTTGTGCTCCGAGTACTTCTTGTACTCCAGTCCGATCTTGTAGCTTGTACCTGCTCCCTGGTGTATTC
270 280 290 300 310 320 330
|||||
TCTTGAACAATGAATACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT
310 320 330 340 350 360 370
|||||
AGGAGTGTGATCACTG-----GTAGGAGATGTTTGTGAATCTTGGTGTATGTTCTGACAAACCTCC
340 350 360 370 380 390 400
|||||
CGG--TGAATCATCTGACCTCTGAGGACACTCAGGAATCAACACGCTGTTGTTTCAATATCTCTCAG
380 390 400 410 420 430 440
|||||
ATCATCCACTCGTAGGAGTCTTCCATCTTGTATCTTGTCCAGACAGTTGTGATGTTGTGATGTTGTG
410 420 430 440 450 460 470
|||||
ATGATCAACATCTCTGACTACATCAATCGGTGATCTTCTGTTACC--ATCACCACATCTGTC-TGAATAC
450 460 470 480 490 500 510
|||||
TCGTTTCTGCTCTGAGCTTACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
480 490 500 510 520 530 540
|||||
TCCAAATCTACATCAACGCGCTCTGATGACCAACCAATCAATCAATCAATCAATCAATCAATCAATCA
520 530 540 550 560 570 580
|||||
TCCAGCAGGATGTTGACACGAGTACTGCGAATCCCTCAGTGAAGTTTCCAGCAGCAGCAGCAGTGGAG
550 560 570 580 590 600 610
|||||
AATAACATCATGTTCAAACTGGAGGCTGTCGTCGACACTCAGCGTGTGATCTGATCTGATCTGATCT
590 600 610 620 630 640 650
|||||
TTCAGTCTGCGTCCGTTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
620 630 640 650 660 670 680 690
|||||
TTCGACAAAGAACTGAACGAAAGAAATCAAGACCTGTACGACAAACAGTCCCAATTCCTGATCTCGAA
660 670 680 690 700 710 720
|||||
GATGTTGTTGATGAGTCCCTCAACACGTC-----GTTTGGCCCA--CATCAGGAACAGACACCTGTG
700 710 720 730 740 750
|||||
GACTTCTGGGTGACTACCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
730 740 750 760 770 780 790 800
|||||
CACACCGCATTCACCTTGTAGCCAGGT---AGGAAAGTAAAGTGTACACCTTGGCACTGTTCTCCAGACG
760 770 780 790 800 810
|||||
GTTGACGTCAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
810 820 830 840 850 860 870
|||||
CCTCTCGA-TTGAACGGGTGAAGTGAAGTCCCT-CCACGTTGTACTCAGCTCTGAGACTCTAGTAGTAG
820 830 840 850 860 870 880
|||||
AACATCTACCTGAACTTTCCTGACCGGTGACCAATTCATCATCAAGAAATACCGCTCTGTAACAAG
880 890 900 910 920 930 940
|||||
TAGGA----GTTCAAGTAGTCCAGTCTCGGTACCGTGTGTGAGAGACTGTATCTCCCTGGGAGGAT
890 900 910 920 930 940 950
|||||
GACATATCGTTCGACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
950 960 970 980 990 1000 1010
|||||
ACCAAT---GCTTCTCAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
950 960 970 980 990 1000 1010
|||||
GATCA-CTTGGTCTACTGACA-CGTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG
1030 1040 1050 1060 1070 1080 1090
|||||
TCTCAGGTAGTGTAAATGAAATCAAGACGACGATGATGATGATGATGATGATGATGATGATGATGATG
1090 1100 1110 1120 1130 1140 1150
|||||
AGGAAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
1100 1110 1120 1130 1140 1150 1160
|||||
AGGAAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
1160 1170 1180 1190 1200 1210 1220
|||||
CTCTCTACAG--TCAAGGGTCTTGTGTACAGGACAT
1170 1180 1190
|||||
CTTCCAACTGGGTACAAATGCTCAGATGCAACGTTCTCTCTGACACTGTGGTTCCTTTG
1230 1240 1250 1260 1270 1280
|||||

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ACCAAT--GCTTCTCAGCGTGGTGTAGAAAGATCTTGTCTGCTCTGGAATCCCGGACGTTGGTAATCTG
1020 1030 1040 1050 1060 1070 1080
1030 1040 1050 1060 1070 1080 1090
GATCA-CITGGTCTACTGACA-CGTGTCTGGTGTAGATACACCTCAGTCTCTCTGTGTGTGTCCTTACGC
1100 1110 1120 1130 1140 1150
TCTCAGTAGTGTATGAATGAATCCAGACGACGAGGTATCATCAATGCAATGA-----ATCTGC
1090 1100 1110 1120 1130 1140 1150
1100 1110 1120 1130 1140 1150
AGGAAGATCTAGTCTTACGCTCACTGATGTCACCGATGAATGCGAGTCACTGT-----CTTACCCAGCAG
1110 1120 1130 1140 1150
AGSACAA---CAATGTACAGATATCGGTTTCATCGTTCACCGATTCACCAATATCGCTAACTGTTG
1160 1170 1180 1190 1200 1210 1220
1170 1180 1190 X
CTCTCTACAG--TCAAGGCTCTGTGTACAGGGACAT
1180 1190
CTTCCAACTGGTACATCTGATGTCGAACGTTCTCTCGCACTCTCGGTTGCTCTTG
1230 1240 1250 1260 1270

US-09-910-186a-23' (1-1200)

US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 28 Optimized Score = 440 Significance = -1.15
Residue Identity = 40% Matches = 539 Mismatches = 647
Gaps = 154 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
TTAGTCTGGAAGCTGTTTACCTTTCCTTTCAGCTTTCGACCTCAGCCAGCAGCAGATGATGTTATGGGA
111 112 113 114 115 116 117
ATGGCTTTCAACAAATATACATCCGAAATCCCTGAACATATCATCTCTGAACCTCGCTTACAAGAC
X 10 20 30 40 50 60
80 90 100 110 120 130 140

GTGATCAGGTTGATCAGTTTGCCTTGGTGTTCGTCGACCTCGTTCAGCTCGTGTGATGACCTTAA--GGC
151 152 153 154 155 156 157
AACAATCTGATGATCTGCTGTTTACGCTGTAAAGTTGAA---GTATACGAGCGGTGTTGAACTGAATGAC
70 80 90 100 110 120 130
150 160 170 180 190 200

AGCATGTTCTTGAACAGTAGTGCAGGACACTCTCGGATGAATCTTT-----GATGTTGTCA
151 152 153 154 155 156 157
AACAACAGTTCAACTGACCTTTCGCTTACTCTTAAGAT--CCGTTTACTCAGATCAGAACATCATCT
140 150 160 170 180 190 200
210 220 230 240 250 260 270

TTGCCCTCCGAGATCTTTCAGCTCCAGACTGTTCTTCAGGTTCTCAACCTGCTCTTGTATGTTCTCC---TTGT
211 212 213 214 215 216 217
TCACTCCGATATCTCGACTCTCTGTTCTCTGATCCGATCCGATCCGAAATACAGAACGAGGTATCC
210 220 230 240 250 260 270
280 290 300 310 320 330 340

CGCTCCGAGTACTTCTTACTCAGCTCGATCTAGCTTGAATTCAGCTCGCTGCTGAGTTC-----
281 282 283 284 285 286 287
AGAATTATCCACAATGAATACACCATCATCACTGCATGAAGATAAATCTGTTGGAAGATCTCCATCC
280 290 300 310 320 330 340
340 350 360 370 380 390 400

-AGGAGTGTGTA-CATCTGGTAGGAGATGTTGTTGAAGTGGGTGATGATCTGGACCAACACCTGCTCCATCA
341 342 343 344 345 346 347
GCGGTAACCGTATCATCTGACTCTGATGATATCAAGGTAAGACCAAAATCTGTATCTTCGAATACAACA
350 360 370 380 390 400 410 420

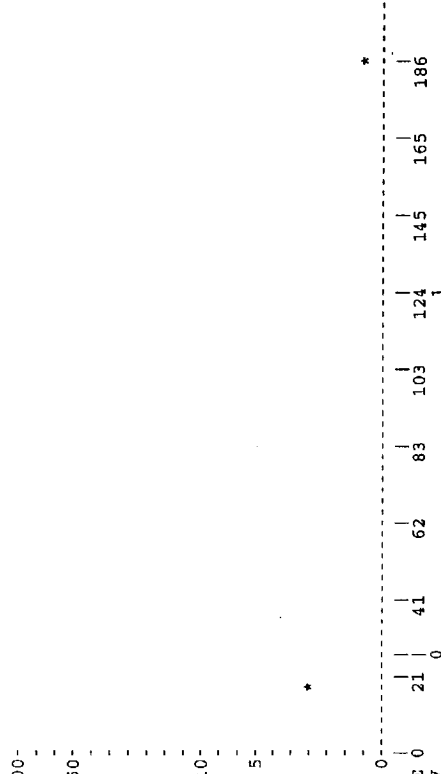
410 420 430 440 450 460
TCC-----ACTCGTAGGAGTCTCTCCATCTCTGATCTC-----TGTCTCAGACAGTGTGCGATGTC
411 412 413 414 415 416 417
TCCGTGAAGACATCTCTGAATACATCAATCTGCTGTTCTGTGTACCATCAACCAATCACTGAAATATGTA
430 440 450 460 470 480 490

470 480 490 500 510 520 530
TTGATGATCTCTGTTCTGCTGAGCTTACTGTAGATCAGGAATGACCCAGCAGGAGTGTGTAATCA

AAATCTACATCAACCGTAAATGGAATCTAATACCGAATCAAAAGACATCC-GTGAAGTTATCGTAAACGGT
500 510 520 530 540 550 560
540 550 560 570 580 590
GGGA-ATGCTCTCCACGAGTGGTCAACACAGTACTGCTGGAATGCCCTCAG--TGAAGT-----TTC
111 112 113 114 115 116 117
GAATCATCTTCAAACTGCGGTGACATCGATCGATCCAGTTTCACTCGGATGAATACTTCTCCATCTTC
570 580 590 600 610 620 630
600 610 620 630 640 650
CAGCAGCACAGT-----TGCAGATGTCAGTGC-GGGTCCGATGTAGGGATGATAGCTGACACAT
641 642 643 644 645 646 647
AACACCGACTCTCTCAGTCAATATCAAGAACGGTACAAAGATCCAGTCTTACTCCGATATACCTGAAAGAC
660 670 680 690 700 710 720
CTGAGATCTTGTCCAGTGTCTCTTACGAGGATGTTGGTAGTGAAGTCTT-CAACACAGCTCTGTTCCACAC
730 740 750 760 770 780 790
TTCCTGGGTAAATCCGCTGATGTACAAACAAGAAATACTATATGTTCAATGCTGGTAAACAAGAACTCTATACATC
710 720 730 740 750 760 770 780
740 750 760 770 780 790
ATCAGAACAGCA-----CCACTTGCACACCGGATTCACCTTGTATGCCAGGTAGGAAGTAAAGTGA--
111 112 113 114 115 116 117
AAACTGAACAAGACTCTCCGCTTGGTGAATCTCTGACTCTTCCAAATACAAACAGAACTCTAAATACATC
790 800 810 820 830 840 850
800 810 820 830 840 850
-----CACCTTGCAGTCTTTCAGAGCTCTCTGATTTGAACGGTGAAGTGAAGTCTCTCCACGTT
111 112 113 114 115 116 117
AACTACCGGAGCTCTACATCGGTGAAAGTTCATATCCGTCGCAAACTTAACCTCAGTCCATCAATGAT
860 870 880 890 900 910 920
860 870 880 890 900 910 920
GTCA-----CTCAGCTCTGAGACTCTAGTAGTA-----GTAGGAG
111 112 113 114 115 116 117
GACTCTGACGTAAAGAAGACTACATCTACCTGACTTTCTCAACCTGAATCAGGAATGGCGTGTATACACC
930 940 950 960 970 980 990
900 910 920 930 940 950 960
TTCAGTACTCCACTCTCTGGTACGGTGTCTGAGAGACTTGTATCTCCCTGGC-AGGATCTCACTCTC
111 112 113 114 115 116 117
TACAAGTCTTCAAGAAGAAGAAAGAGCTTTTCCTGGCTCCGATCTCTGATTCGAGGAACTCTACAC
1000 1010 1020 1030 1040 1050 1060
970 980 990 1000 1010 1020 1030
ACTGTCGATCTAGGCTAGAGCAGCTAGTGTGTC--ATGCTCGAGGTGTTCTTACTGAGGATCACTTGG
111 112 113 114 115 116 117
ACATCCAGATCAAGAATACGACGACCGCTACTCTTCCAGCTCTCTTCAAGAAGATCAAGAA
1070 1080 1090 1100 1110 1120 1130
1040 1050 1060 1070 1080 1090 1100
TCTACTGACACTCTCTGGTAGTAGATCACTCAGTCTCTCTGTTGATGTTCTTACGAGGAGATGTCAT
111 112 113 114 115 116 117
TGTACTG--ACCAATCGTCTGATCGGTATCCACCGTTCCTACGAACTCTGATCTGATTCGAGGAATACA
1150 1160 1170 1180 1190 1200 1210
1110 1120 1130
-----GTCCTCAGCTCAGTGTCTCAGCGATGAATG-----GCAGGTCACTGG
111 112 113 114 115 116 117
AAGACTACTTCTGCATCTCCAAATGCTACCTGAGGAAATTAACGCAAAACCTGACAACTGAACTGGGTT
1220 1230 1240 1250 1260 1270 1280
1160 1170 1180 1190 1200
TTCCTCAGCAGCAGTCTCTACAGTCAAGGCTCTGTTGTACAGGAGAT
111 112 113 114 115 116 117
GCAATGGAGTTCATCCCGAAGAGAGGTTGGACCGAATGAACTCTAGCTGAGGCGCTGAG
1290 1300 1310 1320 1330 X 1340 1350

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IntelliGenetics
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4
Results file us-09-910-186a-24.res made by bobryen on Thu 7 Nov 102 14:36:15-PST.
Query sequence being compared: US-09-910-186A-24 (1-399)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-24 (1-399) with
File : US08123975A.pap



PARAMETERS
Similarity matrix PAM-150
Threshold level of sim. 16%
Match penalty 1
Joining penalty 20
Window size 399
Gap size penalty 5.00
Gap size penalty 0.05
Cutoff score 1
Randomization group 0
SEARCH STATISTICS
Scores: Mean 74 Median 19 Standard Deviation 96.71
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.
The list of best scores is:

Sequence Name Description Length Score Init. Opt. Frame

1. US-08-123-975A-2 Sequence 2, Application U 850 186 263 1.16 0
**** 1 standard deviation above mean ****
**** 0 standard deviation from mean ****
2. US-08-123-975A-3 Sequence 3, Application U 415 19 177 -0.57 0
3. US-08-123-975A-5 Sequence 5, Application U 439 18 175 -0.58 0

1. US-09-910-186A-24 (1-399)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score = 186 Optimized Score = 263 Significance = 1.16
Residue Identity = 34% Matches = 136 Mismatches = 223
Gaps = 1 Conservative Substitutions

MSLYNKTLDRELLVKNLTDLPFGIDISDVKTDFLRKDINEETEVIYVDPNVSDQVILSKNTSEHGQDLL
APGICIDVDNEDLFFIADKNSFSDLSKNEIEYNTQSNYIENDFFINELIITDLSKIELPSE
X 10 20 30 40 50 60 70
80 90 100 110 120 130 140
YPSIDSEILPGENQVFNRTQNVYDLYNSYYLESQKLSDNVEDFTFRSEIEALDNSAKVYTFPP-TLA
NTESLTDENVDPVVEKQPAIKITFTDENTIFOVLYSQTPFLDIRDISLTSSFDALLFSNKVYSFSDMYI
70 80 90 100 110 120 130
150 160 170 180 190 200 210
NKVNAGVOGGLFMWANDVDFDTNLRKTDLDKISDVSAIPYIGPALNINSVRGNFTFAFVGTVI
KTANKVVEAGLFAGVVKQIVNDFVTEANKSNTMDKIADISLIVYIGLALNVGNETAKGNFENAFIAGASI
140 150 160 170 180 190 200
220 230 240 250 260 270 280
LLEAPPEITPAGLGFVYISKVORNEIITKDNCLEQRKRWKDSYERWGTWLSRITQFNISYQMVDS
LLEFPELLIPVVGAFLESYIDNKNKIITIDNALTKRNEKSDMYGLIWAQVLSVNTFOYTIKEGYKA
210 220 230 240 250 260 270 280
290 300 310 320 330 340 350
LNYQAGATKAKIDLEYKKSQSDKENIKSQVENLKNISLDYKISEAMNNINKFIRECSVTYLFKNMLPKVIDE
LNYQALEEIKYINYYSEKESKNINIDFNINSKLNKNGINQAINNFINNGSVSYLMKMKIPLAVEK
290 300 310 320 330 340 350
360 370 380 390 X
LNEFDNRTKAKLINLIDSHNLIYGEVDKAKAVNNNSFN
LLEFDTLKNLKYIDENKLYIGSAEYKSKVNYKYLKIMPFDSLIIYTDILILEMFN
360 370 380 390 X 400 410

2. US-09-910-186A-24 (1-399)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score = 19 Optimized Score = 177 Significance = -0.57
Residue Identity = 7% Matches = 30 Mismatches = 342
Gaps = 6 Conservative Substitutions

X 10 20 30 40 50 60 70
MSLYNKTLDRELLVKNLTDLPFGIDISDVKTDFLRKDINEETEVIYVDPNVSDQVILSKNTSEHGQDLL
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLENLSSKIEVLKNAIVYNSYENFSTFWIRIPKY
X 10 20 30 40 50 60 70
80 90 100 110 120 130 140
YPSIDSEILPGENQVFNRTQNVYDLYNSYYLESQKLSDNVEDFTFRSEIEALDNSAKVYTFPP-TLA
FNSISLNNEYTIINCMENNSGWKSYLNKYGELIWTQDQIKQVRYFKYSQMI--NISDVINRWIETITNN
80 90 100 110 120 130 140

FIPKDEGWE
430

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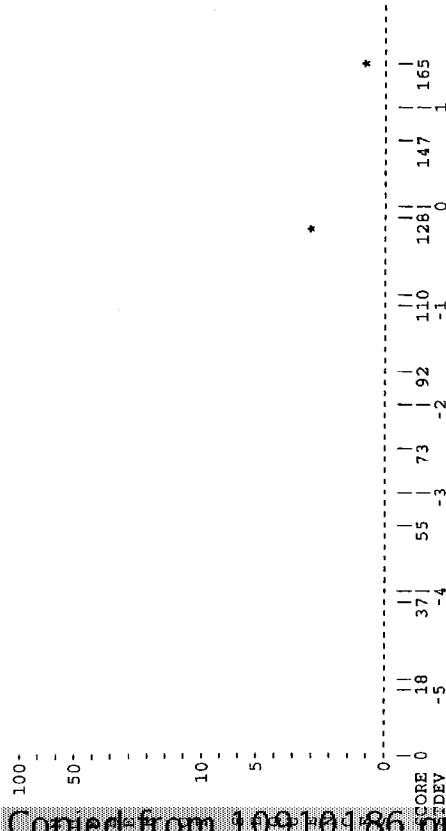
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-25.res made by bobryen on Thu 7 Nov 102 14:48:41-PST.

Query sequence being compared: US-09-910-186A-25 (1-1161)

Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-25 (1-1161) with:
File: US08123975A.seq



PARAMETERS

Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap size penalty 5.00 Window size 500
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
139 127 22.52
Times: CPU 00:00:00.00
Total Elapsed 00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Frame
1. US-08-123-975A-6	Sequence 6, Application U	1351	165	453	1.15 0
2. US-08-123-975A-4	Sequence 4, Application U	1338	126	443	-0.58 0
3. US-08-123-975A-1	Sequence 1, Application U	1338	126	443	-0.58 0
1. US-09-910-186A-25	(1-1161)				
US-08-123-975A-6	Sequence 6, Application US/08123975A				
Initial Score	= 165	Optimized Score	= 453	Significance	= 1.15
Residue Identity	= 43%	Matches	= 528	Mismatches	= 610
Gaps	= 88	Conservative Substitutions	= 0		
X	10 20 30 40 50 60 70				
ATGGCAACTCCGTCGACGACTCCACCTGCATCAAGTCAAGAACACACAGACGTCCTATAGTTGGCGACAA-					
ATGGCTTCAACAAATCAATTCGGAATCCTGAACATATCATCTCGAACCTCGGTACAAAGACAAAT					
X	10 20 30 40 50 60 70				
80 90 100 110 120 130					
GGACTCCATCCCGAGG---AGATCTTCGAGAACAGATCATACCCGACGAGACC--AACGTTCAAACTAC					
CTGATCGATCTCTCGGTACGGTCTAAAGTTGAAGTATACGACGCTGTGAAGTGAATGACAGACAGACGAG					
80 90 100 110 120 130 140					
140 150 160 170 180 190 200 210					
TCCGACAAATTTCTTTTGGACGAGTC---CATCTGGAGGTCGAGTCCCAATCAACCCAGAGATCTCGAC					
TTCRAACTGACCTCTTCGCTAACTCTAAGATCGGTCTACTCAGATCAGACATCATCTTCACTCCGTA					
150 160 170 180 190 200 210					
210 220 230 240 250 260 270					
CCACTGTTCCCAAGCTCAACATGGAGCCATTAATGTCAGGTGAGGAGATCGTCTCTAGCAGGACATC					
TTCCTGGACTCTCTGTTCTCTTGGATCGGTATCCGGAATACAGACGAGGATTCAGAAATATACATC					
220 230 240 250 260 270 280					
280 290 300 310 320 330 340 350					
ACCAAGTACGTGACTACTTGAACCTCTACTACTTGGAGTCTCAAAAGTTGTCTAACAAGCTGGAGAAC					
CACAATGAATACACCATCATCAACTGCATGAAGATAACTCTGTTGGAAGATCTCCATCCGCGGTATACCGT					
290 300 310 320 330 340 350 360					
360 370 380 390 400 410 420 430					
ATCCTTTGACACACCTCGTCGAGAGGCTTGGTTACTCTAACAAGATC---TACACTCTCTCCCATCC					
ATCATCTGACTCTGATCGATATCAAGGTAAGACCAATCTGTATTCTCGAATACAAATCCGTGAAGAC					
370 380 390 400 410 420 430					
430 440 450 460 470 480 490					
TTGGCTGAGAGAGTTAAACAGGTTTCAAGCTGTTTGTCTGAACTGGGCCACGAGGTCGTCTGAGGAC					
ATCTCTGAATACATCAA-----TCGCTGG-TTCTCGTACCATCACCATAACCTGAAGATG--					
440 450 460 470 480 490					
500 510 520 530 540 550					
TTCACCAACACATCATGAAGAGACACCTCGACAGATCTCCGAGCTCTCCGTCTATCCCATATC					
-----CTAAATCTACATCAGCGGTAACTGGAATCTAATACCGACATCAAGACATCCGTGAAGTTATC					
500 510 520 530 540 550					
570 580 590 600 610 620 630					
GGTCAGGCTTTGAACATC-GGTAACTCCGCTCGAGAGGTAACTTCAACCCAGGCTTCGCCACCGGNGT					
GCTAACGGTGAATCATCTTCAACTGCGTGCATCGATCGT-ACCCAGTTCTCATCTCGATGAATACTT					
560 570 580 590 600 610 620					
640 650 660 670 680 690 700					
CGCCTTCCTGCTGGAGGTTTCCAGAGTTTCAACATCCAGCCCTGGGTGTCTTCACTTCTACTCTCCAT					

-----ACGACGACAAAGCTTCAAAAGCTTACTTCGACAAAGTCTCTTTTGACAGAGTCCAACTCTCGACAGCGTG
AAGTTAACTTCGATCCGGATCGACAAAGATCAGATCCAGCTGTCTAACTCTGGAATCTTTCCAAAATTCGAAGTT-
150 160 170 180 190 200 210
180 190 200 210 220 230 240 250
AGGTCCCAATCAACCCAGAGATCGTCGACCCACTGTGCGCAACGCTCAACATGGAGGCATTTGAATTCGCCAG
--ATCTTGAGGAATCGTATCCGTATACAACTCTTAATGACGAAACATCTCCCA---CCTCTCTCTGGATTCGGTA
220 230 240 250 260 270
260 270 280 290 300 310 320 330 340 350
GTGAGGAGATCGCTCTCTACGACGACATCCCAAGTACCTCGACTACTTGAATCCCTACTACTCTTGGAGT
TCCCGAAATACTTCACTCCATCTCTCTGACAAATGAATACACCATCATCACTGCGATGGAACAACTATCTG
280 290 300 310 320 330 340 350
330 340 350 360 370 380 390 400 410 420 430
CTCAAAAGTGTGTAAACAACGTCGAGAACATCACTTGAAC-----CACCTCCGTCGAG-----G
GTTGGAAGTATCTCTGAACTACGCTGAATCATCTGGACTCTGACGAGCACTCAGAAATCAACACAGCGTG
360 370 380 390 400 410 420 430
380 390 400 410 420 430 440 450 460 470 480 490 500
AGCGCTTGGGTACTCTAACAGATCTACACCT-----TCCCTGCCATC-----CTTGCTCAGAAGGTTA
TT
TTGTATTCAAAATACCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTACCATCAACCA
430 440 450 460 470 480 490
440 450 460 470 480 490 500
ACAGGGTGTTCAGCTGGTTGTCTGAACTGGCGCAACAGAGTCTGTCAGAGCTTTCACCAACCAATCA
TT
ACAATGGTGAATTAATCTCCAAAATCTACATCAACAGCGCGTCTGATCGACAGAAACCGATCTCTCCAACTGG
500 510 520 530 540 550 560
510 520 530 540 550 560 570
TGAGAGAGACACCTGGACAGATC-----TCGAGTCTCGTCTATCATCCCATACATCGGTCCAGC-----
GTAAATCCACGCTCTTAATTAACATCATGTTTCAAACTGGACGGTGTGCTGACACTCACCGCTACATCTGGGA
570 580 590 600 610 620 630
580 590 600 610 620 630
-----CTTGAACATCGGTAACCTCCGCTTGAGAGGTAACTTAAC-CAGGCGTTCGCCACCGCGGT-----
TT
TCAATATCTCAATCTGTGACAAAGACTGACCAAAAGAAATCAAGACCTGTACGACACACAGTCCA
640 650 660 670 680 690 700 710
640 650 660 670 680 690 700 710
-----GTCCCT-----TCTGTCTGGAGGTTTCCC-----AGAGTTCACTCCACCTCCAGCCCTGG
ATTTCTGGTATCTGAAGACTTCTGGGTGACTACTCTGACTGAGTCAAGCAAAACCGTACTACATCTGCTGAATCTGT

GTGTCCTTACCTTCTAC-----TCCCTCATCCAGGAGAGAGAAGATCATCATCAAGACCATTGCGAAGCTGTGTTG
ACGATCCGACAAATACCTTCACGCTCAACATGTAGTATCCGCGGTTCATGTACTGTACCTGAAGAGTCCGCGGTG

[illegible]

880 890 900 910 920 930
A-----CQGCATCAAGGCCAAGATCGACCTGGAGTACAAGAGTACTCCGGTTCGACCAAGGAGA

[illegible]

Copied from 109-10186 on 05-05-2004

AGTTATCCCGGTGATGACGGTTGGGGTGACGTCGCTGTAAACCGG
1290 1300 1310 1320 1330

640 650 660 670 680 690 700

```

Initial Score      = 32  Optimized Score = 246  Significance = -1.11
Residue Identity  = 40%  Matches       = 292  Mismatches  = 384
Gaps              = 51  Conservative Substitutions = 0

```

X 10 20 30 40 50
 TTAGTCACTCACCACCGAGTGTGTGGAGTCACAGTTGATC
 |||||
 ATCTCAACACCGAAGTGTCTAGTCGATATCGAAGACGTCACAGTCTATCTCGAATACCTG
 640 650 660 670 680 690 700

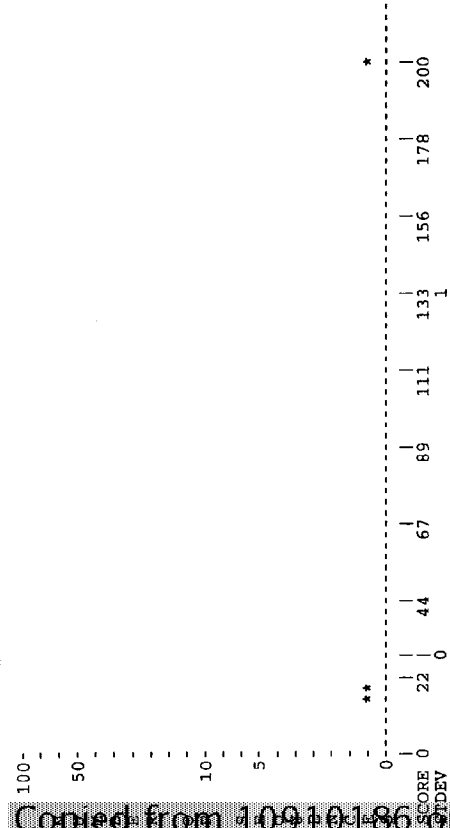
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0| 10
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-26.res made by bobryen on Thu 7 Nov 102 14:36:40-PST.

Query sequence being compared: US-09-910-186A-26 (1-386)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-26 (1-386) with:
File: US08123975A.pep



PARAMETERS

Similarity matrix PAM-150
Threshold level of sim. 16
Mismatch penalty 1
Gap penalty 5.00
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 78 Median 17 Standard Deviation 105.38
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Frame
1. US-08-123-975A-2	Sequence 2, Application 0	950	200	262	1.16
2. US-08-123-975A-3	Sequence 3, Application 0	415	19	170	-0.56
3. US-08-123-975A-5	Sequence 5, Application 0	439	16	101	-0.59

1. US-09-910-186A-26 (1-386)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score = 200
Residue Identity = 37%
Gaps = 2
Optimized Score = 262
Matches = 143
Significance = 1.16
Conservative Substitutions = 29

X 10 20 30 40 50 60 70
MANSRDSSTCIKVNRLPYVADKDSIQEIFENKIITDETNYQNSDKFSLDESILDGQVPINPVDPLL
APGICIDVDNEDLFFIADKNSFSDLSKNERIEYNTQSNYIENDFPINELILDLDLISKIELPSENT
X 10 20 30 40 50 60
80 90 100 110 120 130 140
PNVNMELNLPGEIVFDDITKYVDYLSVYVLEOKLSNNVENITLATSVEEALGYKNKIYTFPLP-SLAE
ESLTDNFVDVPVEKQ-PAKKIETDENTIFQVLYSQTFFLDIREDISLASSDDALLFSNKVYSFSDMYIK
70 80 90 100 110 120 130
150 160 170 180 190 200 210
KVNKGVOAGLFNMANEVEDFTTNIMKDTLQKISDVSIPIYIGPALNIGNSALRGNFQAFAGVAFV
TANKVVEAGLFAGWVKQIVNDEFTJEANKSNTMDKIADISLIVPYIGLNVGNETAKGNFENAFAGASIL
140 150 160 170 180 190 200 210
220 230 240 250 260 270 280
LEGPEFTIPALGVFTTYSIQEREKIITKIECNLEQVRKWDKSDQWVSNWLSRITTFQFNINQMTDLSL
LEFTELPVVGAFLESYIDNKNKIITKDIALTKRNEKWSMDGLIYVAQWLSVTQFTYIKREGMYKAL
220 230 240 250 260 270 280
290 300 310 320 330 340 350
SYQADAKAKIDLEKYSKSDKENIKSOVENKNSLDVKISEAMNNINKFIRECSVYLFKKNLKPVIDEL
NYQAALEELIKYRNIYSEKESNINDFNINSKLENGINQAINNNFINGCSVYLMKMKPLAVEKL
290 300 310 320 330 340 350
360 370 380 X
AKFDLRTKTELINLIDSHNIIIVGEVD
LDFDNTLAKNLLNIDENKLYLSAEYKSKVKNKYKLTIMPFDLSI
360 370 380 390 400

2. US-09-910-186A-26 (1-386)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score = 19
Residue Identity = 11%
Gaps = 9
Optimized Score = 170
Matches = 44
Significance = -0.56
Conservative Substitutions = 28

X 10 20 30 40 50
MANSRDSSTCIKVNRLPYVADKDSIQEIFENKIITDETNYQNSDKFSLDESIL
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIOLFNLKESKIEVLKNAIVNSMYENESFWRIRPKYF
10 X 20 30 40 50 60 70
60 70 80 90 100 110 120
DQGVFINPEIVDPLLPVNMELNLPGEIVFDDITKYVDYLSVYVLEOKLSNNVENITLATSVEEALG
NSISLNNEVTTINCMMNSGKVSINNGEIIWLODQEIQRVVRKYSQMINISDYINRWIVTITNNRLN
80 90 100 110 120 130 140

AAAGACCTGGACCGAGGTCAATCCATAACTTCAACTCCGAGTCCGGCCCTGTGTCTCCGACGAGAAAGCTGAA
50 60 70 80 90 100 110
ACATCATCAATACC--TCCATCTCGAACCCTGCCTACGAAT---CCAATCACCTGATGACACCTGTCTCGCTA
120 130 140 150 160 170 180
CGTTTCCAAATCAACATCGGTTCTTAAGATTAACTTCGATCGAGTCCGACGAAGATCAGATCCAGCTGTTCCTAA
190 200 210 220 230 240 250
CGTTAAGAGCTTAACGCTTCTTCTACTTAGACGCTCAGAAGGTCCGCGAGGTGAGAAC---AAGCTCAA
260 270 280 290 300 310 320 330 340
TCTGGAACTCTCCAAATCGAAGTTATCTCTGAAGATGCTATCGTATACACTCTATGTAGGAACAACTCTCTC
350 360 370 380 390 400 410
TCTCACTCTTCAATGACACAGCGCTGTGGAGACGCTAAGATCTACACCTTCTTCTCCTCCGAGTTCAT
420 430 440 450 460 470 480
CACACGCTCAACAGCTGTGAGGCGCGATGTT--CGTAAGCTGATTTCACGAGCTTTAGTAGACTTC
490 500 510 520 530 540 550
ACTACTGAGGCTTAACCAAGTCCACTGTTGACAAGATCGGTGACATCTCATCGTCTGTCCTCCATACATCGGT
560 570 580 590 600 610
--CTGGCTC---TGACATCGGACGAGCGACAGAAGGGC-----AACTCAAGATGCGCCTTGAG--TT
620 630 640 650 660 670 680
GTTGGTCCGGGTATTTGTTGGAGTTCGAACCCGAGCTGTGATCCCTACCTCTGCTTCTTCACGATCA
690 700 710 720 730 740 750
GACCAAGAACCGATCCCAATCTGTGGTAACATCCAGCTTCATA---TAACATCATGTTTCAAACTGACGG
760 770 780 790 800 810 820
TTGTGCTGACACTCACCGCTACATCTGGATCAATACTTCAATCTGTTTCGAAAGAACTGACGACGAAGA
830 840 850 860 870 880 890
GTCCTTCTGGGTTCTCCGACACACAGACAGGTCATTAGGCGCATCAACACGCGCTTGAGGAGCGTGA
900 910 920 930 940 950 960
AATCAAGACCTGTACGACACACAGTCCCAATTTCTGTATCTCCGTAAGAACTTCTGGGTGTACTACTCTGCAGTA
970 980 990 1000
----CCGAAGATGGAAGAACTATTCTTCACTGCTCGCAACTGGATGACCAAGATCAACACC--CAAGTT
1010 1020 1030 1040 1050 1060 1070
AATCAAGACCTGTACGACACACAGTCCCAATTTCTGTATCTCCGTAAGAACTTCTGGGTGTACTACTCTGCAGTA

US-08-123-975A-4 Sequence 4, Application US/08123975A

CGCAACCGTACTACATGCTGAATCTGTACGATCCGAACAATAACGTTGACGTCACAATGTAGTATCCG
760 770 780 790 800 810 820

CGAGTCCAAGGTACAACTCCTACACCCTGGAG-**TTCGAGAACAAGCGTGTTACCAACAAGTAGCATATCAA**

A-**TCCGCATTACTATTAATAAAGAACGGAATGAGCTGCTGAGTATGAGTATGAGTACCAACAATCTTACCGTAAGCTTTCCTCTG**

960 970 980 990 1000 1010 1020
 CAGATCGAGAACGAGCTGAACACAGAGGTCTCCATCGCCATGAACAACATCGACA -GGTTCTGACCGAGTC

810	820	830	840	850	860
-----	-----	-----	-----	-----	-----

$\begin{matrix} \text{X} \\ \text{CAT} \\ | \\ \text{CGAC} \\ 11 \end{matrix}$

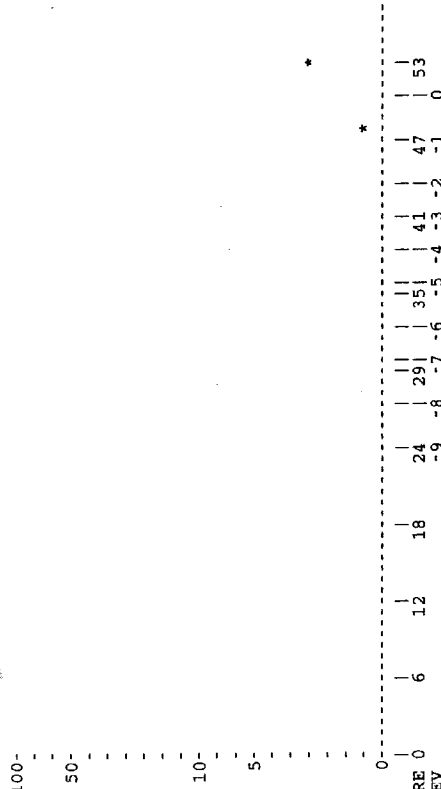
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-29.res made by bobryen on Thu 7 Nov 102 14:49:57-PST.

Query sequence being compared: US-09-910-186a-29 (1-1227)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186a-29 (1-1227) with
File: US08123975A.res



PARAMETERS

Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 5.00 Window size 500
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 51 Median 49 Standard Deviation 2.89
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig. Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	53	412	0.69
2. US-08-123-975A-1	Sequence 1, Application U	1338	53	412	0.69
3. US-08-123-975A-6	Sequence 6, Application U	1351	48	412	-1.04
1. US-09-910-186A-29	(1-1227)				
US-08-123-975A-4	Sequence 4, Application US/08123975A				
Initial Score	= 53	Optimized Score	= 412	Significance	= 0.69
Residue Identity	= 41%	Matches	= 499	Mismatches	= 633
Gaps	=	Conservative Substitutions	=		
50	60 X	70	80	90	100
110	120	130	140	150	160
170	180	190	200	210	220
230	240	250	260	270	280
290	300	310	320	330	340
350	360	370	380	390	400
410	420	430	440	450	460
470	480	490	500	510	520
530	540	550	560	570	580
590	600	610	620	630	640
650	660	670	680	690	700
710	720	730	740	750	760
770	780	790	800	810	820
830	840	850	860	870	880
890	900	910	920	930	940
950	960	970	980	990	1000

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GGAGGTTGCTGTCGACACTCACCCTACAT-CTGGATCA--AATCTTCAATCTCTTCGACAAAGAACTGAA
610 620 630 640 650 660 670
760 770 780 790 800 810 820
TGATCGAAAGAGAGGCTAAGTGAAGCAATCTACTCATGATTTATCAAACTGCTTACTAGAAATTA--A
CGAAAGAAATCAAGAGCTGTACGACACACAGTCCCAATCTGATATCCCTGAAGAGCTTCTGGGGTACTA
680 690 700 710 720 730 740
CACTCATTTAAACAAGAGAGGAGGAGCAATGTACCAAGGCTTCGCAAAAGTGGATGCTATCAAGACTGC
830 840 850 860 870 880 890
CTGTGAGTACGACAAACCGTACTACATGCTGATCTGTACGATCCGACAAATATGAGTTCACAAATGT
750 760 770 780 790 800 810
AATT-----GAATACAAAGTACCAAACTATAC-----TTCCGATGAGAAGAACAGACTTGAATCTGAATAC
900 910 920 930 940 950
AGTATCCGGGTTACATGTACATGTACCTGAAAGGTCGGGTCTGTTGATGACTACCAACATCTACTGA--AC
820 830 840 850 860 870 880
AATATCAACAACTTGAAGAGTGTGAACAGAAAGTTCTTTGGCTATGAAGAAATATCAAGAAATATATG
960 970 980 990 1000 1010 1020
ACCGA--ATCCTCTATCTTACTGTATGAAGTT--GATCAATAGGCGCAAGTTGGTGAAGTGAAGATTA
1030 1040 1050 1060 1070 1080 1090
AACAATATCGTGAT--ACATCAATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
970 980 990 1000 1010 1020 1030
CGATACCAACGTTAAGAGGATCTGTGATACATCTTCGACACAG--ATCAATC-CTGGGAGAGCAGAC
1100 1110 1120 1130 1140 1150 1160
GGCTGTGTGAAGAGATCTGTCTGCTGGAATCCCGGACGTTGGTAATCTCTCAGGTATGTGATAT
1040 1050 1060 1070 1080 1090 1100
AAAGAGCTGAGTGTATTTGGTACTTCCACTTTGAACTCTCCATTCCTTACCTTTGCTTTAA
1170 1180 1190 1200 1210 1220
GAAATCCAAAGACGACGAGGTA--TGATCAAAATGCAAAATGAATCTCGAGGACAAAGTGGTACGA
1110 1120 1130 1140 1150 1160 1170
TATCGTTTCAT
1180

```

US-09-910-186a-29 (1-1227)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 53 Optimized Score = 412 Significance = 0.69
Residue Identity = 41% Matches = 499 Mismatches = 533
Gaps = 64 Conservative Substitutions = 0

```

TTATTTCTTTCGCTCCGAGTCAAGCTACAGAGAGATAT--TAACACACCTTAAGAGATTCAGATAC
50 60 X 70 80 90 100 110
TACCACTTAACAACTACCGGAACTTGGATGAGTTATTTGGATTAACAACTACAGACCATCC
120 130 140 150 160 170 180
CAATATACCTTCACTCTGAACTTGGCTAC---GAACTCAATCACTGATGACCTCTCTCGCTACGCTTC
60 70 80 90 100 110 120
TCAAATTTCCAACTGACCTTAACAACTTGTTCAGAGCAAC--TCCTACCTTCCAGATACGATTTCAAC
190 200 210 220 230 240 250
CAAAATCAACATCGGTTCTAAAGTTAACTTCGATCGATCGACAGAAATCAGATCCAGCTGTTCACT--G
130 140 150 160 170 180 190

```

TTGGAGTTGTTCAGAACTTACCACTCTGTCAATTTAGTTTTACGATCAAGTCTACATCGATTTCATAC

ATCAAGACATCCGCTGGAGATTACGCTTAACCGTGAATCACTTCCAACTCGACGCTGACATCCATCGCTAC	540	550	560	570	580	590	600
GAGACA--AGATAAAGCAATTAAAGCTATTAA-----CAACTCCTTGATCGAAGAGAGGCTAAGTGGAA	720	730	740	750	760	770	
CAGTTCACTGGATGAATACTTCCACTTCCACACCGACTCTCTCACTCCAAATCGAAGAA--CGGTA	610	620	630	640	650	660	670
780	790	800	810	820	830	840	
GGAAATCTACTCATGGATTGTATCAAACTGGCTTACT--AGAAATTAACACTCAATTTAAACAAGAGAAAGAG							
CAAGATCCAGICTTACTCCGAAT--ACCTGAAGAGACTTCTGGGTAAATCCGCTGATGTACAACAAGAATAAC	580	590	600	610	620	630	640
850	860	870	880	890	900	910	
CRAATGTACCGAGCTCGCAAAACCAAGTCGATGCTATCAAGACATGCGAATTGAATACAACTACAACACTAT							
TATATGTTCAATGCT--GGTACAAGAATCT--TTAATCAAACTGAAGAAAGACTCTCCGGTTGGTGAATC	750	760	770	780	790	800	810
920	930	940	950	960	970	980	
ACTTCGGATGAGAAGACAGACTTGAATCTGATCAATATCAAC-----AACATTGAAGAGAGCTTG							
CTGACFCGTCGCAATACACAGAACTCTAAATCACTTAAATCACTACCGGACCTGTTACATCGGTGAAGATTC	820	830	840	850	860	870	880
AACA-----AGAAAGT----TTCTTGGCTATGAAGAATATCGAAGATTTTACCGCAATCTCTATCTCT	990	1000	1010	1020	1030	1040	
ATCATCCGTCGCAATCTAATCTCTCACTCCATCAATGATGACATCGTACGTAAGAAGACTTACATCTACCTG	890	900	910	920	930	940	950
1050	1060	1070	1080	1090	1100	1110	
TACTTGATGAAGTTTATCAATGAGCGCAAGTTGGTAAAGTTGAAGAAGTACGATTAACCGCTTAAGAGCGAT							
GACTTCTCAACCTTGAATCAGAAATGCGGTGTATACACCTACAAGTACTTCAAGAAGAGAGAAGAAAGCTT	960	970	980	990	1000	1010	1020
1120	1130	1140	1150	1160	1170	1180	
CTGCTGAATCAATCTTCGACACAGATCAATCTCGGAGAGACAGACAAAGCGCTGAGTGATTTGGTTACT							
TTCTCG--GCTCCGATCTCTGATTCGGACGAATCTACAACACCATCCAGATCAAGAA--TACGACCAAGACG	1030	1040	1050	1060	1070	1080	1090
1190	1200	1210	1220	X			
TCCACTTTGAATCTCTCCATTCATTTGAGCTTTCTTAA							
CCGACCTACTTGGCAGCTGCTGTTTCAAGAAGATGAAGAATCTACTGACGAAATCGG	1110	1120	1130	1140	1150		

TCGAATCACTGATCGACCTGTCCTGGCTACGGTTCACAAAATCAACATCGGTTCTAAAGTTAACTTGAATTCGGATCCG

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

ATGGCTCTTAAAGTGGT---ATGCTACTCTTCAACTACCAAACTGCGCTCAT--TGATCAACTTCATC

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

ATGACAAAGAATCAGATCCAGCTGTTCAACTTGGATCTTCCAAATCGAGTTATCTCGAAGTATCTCGAAGATCTATC

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

AACTAGAGATAGAGATCCGGTCAATAAATCTTTCCGATATCTTCATAGCCAAAGAACTTTCTTGTTCACAC

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

GTATACAACCTATATGACAAAATCTTCCACCTCTCTCGATCGATTCGATCGATTCGGAATATCCGAAATACTTCAACTCCATC

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

TCCTCTCAATCTGTCGATATTCAG-ATTCAGTCTGTTCTTCATCGGAAGTAGTTGTTGT

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

TCCTGAAATATGAAATACACCATCATCAACTGATGGAACAAATCTTGGT--TGGAAGATCTCTCGAACT

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

AC-TTGTATTCAATTCGAGTCTTGATAGCATCGACTTGGTTTCGAGAGCCTGGTA--CAATTCCTC----

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

ACGGTCAATCATCTGGAATCTGCAGACACTCAGAAATCAACAGCGTGTGTATCCAATCTCTCAGA

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

-----CTTTCCTTGTAAATCAGTGTAAATTCAGTAAGCCAGTTTGATACAATCCAGTAGAT-TT

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

TGATCAACATCTCTGACTACATCAATCGCTGGATCTTCCTACCATCACCACAATCGTCTGAAATCACTCCA

120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 3

US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	36	Optimized Score	=	455	Significance	=	0.87
Residue Identity	=	42%	Matches	=	549	Mismatches	=	651
Gaps	=	98	Conservative Substitutions	=			=	0

X
 10 20 30 40
 TTAAGAACCTCAATGGATGGAGAGTTCAAGTGA-----AGTAA
 CGCTGCTGTCTACCTTCATGATACATCAAGACATCATCAATACCTCCATCTCTGAACCTGGCTGACGAA

50 60 70 80 90 100 110
CCCAATCAC-----TCAGCTCGTTGTCTGCTCTCCAGATTGATCTGTGSTCGAGAATGTAGTTC-AGCAG

[illegible]

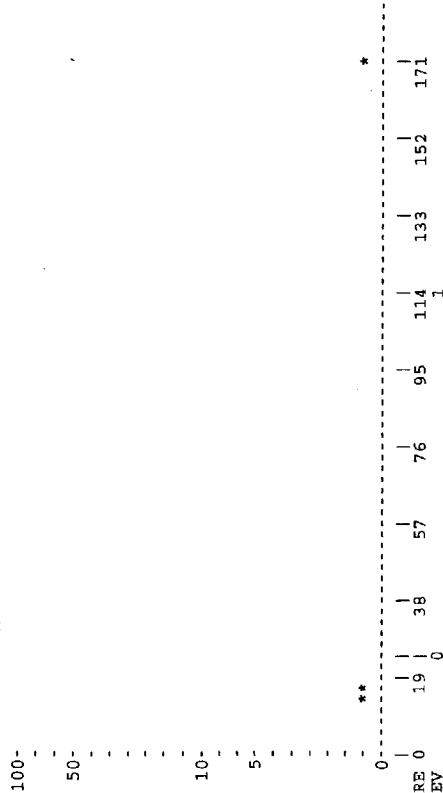
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-30.res made by bobryen on Thu 7 Nov 102 14:37:36-PST.

Query sequence being compared: US-09-910-186A-30 (1-408)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-30 (1-408) with:
File: US08123975A.pep



PARAMETERS

Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 16%
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 408
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 67 Median 15 Standard Deviation 89.51
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Init. Opt. Frame

1. US-08-123-975A-2 Sequence 2, Application U 850 171 276 1.16 0
**** 1 standard deviation above mean ****
**** 0 standard deviation from mean ****
2. US-08-123-975A-3 Sequence 3, Application U 415 18 174 -0.55 0
3. US-08-123-975A-5 Sequence 5, Application U 439 14 134 -0.59 0
1. US-09-910-186A-30 (1-408)
US-08-123-975A-2 Sequence 2, Application US/08123975A
Initial Score = 171 Optimized Score = 276 Significance = 1.16
Residue Identity = 40% Matches = 165 Mismatches = 202
Gaps = 8 Conservative Substitutions = 32

X 10 20 30 40 50 60 70
MAPRLCIRVNSSEFFVASESSYNENDINTPEKIDDTNLNNYRNRLDEVILDYNSQTIPQISNRLNTL
APGICIDVDNEDLFFIADKNSFSDLLSKNERIEYNTQSNVIENDFPINELLDTDLISKIELPSENTESL
X 10 20 30 40 50 60 70
80 90 100 110 120 130 140
VQNSYVPRYDSNGTSEIEEYDVDFNVFFYLHAQKPEGETNISLTSIDTALLESKD-IPFSEFIDTI
TDENVDPVYKQPA--IKKIFTDENTIFQYLYSQTFFLDIRDISLTSFDDALLFSKNKYVSFFSMDYKTA
150 160 170 180 190 200 210
NKPVNAALFIDWISKVIRFTTEATCKSTVDKIDISLIVPVGLALNIIIEAKGNFEAFELLYGVILLE
NKYVEAGLFAGWVKQIVNDFVIEANKSNTMDKIDISLIVPVGLALNIIIEAKGNFEAFELLYGVILLE
150 160 170 180 190 200 210
220 230 240 250 260 270 280
FYPELIPVILVFTKSYSDSVENKKAIAKAINSLIEREAKWKIYIWSNWLTRINTOFNKKQMQQA
FIPPELLIPVAGFLSEYID--NKNKIITIDNALTNRNEKWSMDYGLIVAQWLSTVNTOFFYIKEGMYKA
290 300 310 320 330 340 350
LQNOVDAIKATAYKYNNYTSDEKNRLESEYNNIEELANKYSLAMKNIERFETESSYSLMKLINEAKV
LNQAOALEEIKYRNIYSEKESNINIDF--NDINSKLEGINQADINNFINGCSVSLMKKMIPLAV
360 370 380 390 400 X
GKLKYNHVKSDLLNYILDHRSILGEQTNELSDLVSTLNSIPFELS
EKLLDFDNLKKNLLNYIDENKLYLIGSAEYKSKVNYLKTIMPFDLSIYNTDITILEMENKYNSEIL
360 370 380 390 400 410 420

2. US-09-910-186A-30 (1-408)
US-08-123-975A-3 Sequence 3, Application US/08123975A
Initial Score = 18 Optimized Score = 174 Significance = -0.55
Residue Identity = 9% Matches = 36 Mismatches = 330
Gaps = 2 Conservative Substitutions

X 10 20 30 40 50 60 70
MAPRLCIRVNSSEFFVASESSYNENDINTPEKIDDTNLNNYRNRLDEVILDYNSQTIPQISNRLNTL
APGICIDVDNEDLFFIADKNSFSDLLSKNERIEYNTQSNVIENDFPINELLDTDLISKIELPSENTESL
X 10 20 30 40 50 60 70
80 90 100 110 120 130 140
VQNSYVPRYDSNGTSEIEEYDVDFNVFFYLHAQKPEGETNISLTSIDTALLESKD-IPFSEFIDTI
TDENVDPVYKQPA--IKKIFTDENTIFQYLYSQTFFLDIRDISLTSFDDALLFSKNKYVSFFSMDYKTA
150 160 170 180 190 200 210
NKPVNAALFIDWISKVIRFTTEATCKSTVDKIDISLIVPVGLALNIIIEAKGNFEAFELLYGVILLE
NKYVEAGLFAGWVKQIVNDFVIEANKSNTMDKIDISLIVPVGLALNIIIEAKGNFEAFELLYGVILLE
150 160 170 180 190 200 210
220 230 240 250 260 270 280
FYPELIPVILVFTKSYSDSVENKKAIAKAINSLIEREAKWKIYIWSNWLTRINTOFNKKQMQQA
FIPPELLIPVAGFLSEYID--NKNKIITIDNALTNRNEKWSMDYGLIVAQWLSTVNTOFFYIKEGMYKA
290 300 310 320 330 340 350
LQNOVDAIKATAYKYNNYTSDEKNRLESEYNNIEELANKYSLAMKNIERFETESSYSLMKLINEAKV
LNQAOALEEIKYRNIYSEKESNINIDF--NDINSKLEGINQADINNFINGCSVSLMKKMIPLAV
360 370 380 390 400 X
GKLKYNHVKSDLLNYILDHRSILGEQTNELSDLVSTLNSIPFELS
EKLLDFDNLKKNLLNYIDENKLYLIGSAEYKSKVNYLKTIMPFDLSIYNTDITILEMENKYNSEIL
360 370 380 390 400 410 420

2. US-09-910-186A-30 (1-408)
US-08-123-975A-3 Sequence 3, Application US/08123975A
Initial Score = 18 Optimized Score = 174 Significance = -0.55
Residue Identity = 9% Matches = 36 Mismatches = 330
Gaps = 2 Conservative Substitutions

X 10 20 30 40 50 60 70
MAPRLCIRVNSSEFFVASESSYNENDINTPEKIDDTNLNNYRNRLDEVILDYNSQTIPQISNRLNTL
APGICIDVDNEDLFFIADKNSFSDLLSKNERIEYNTQSNVIENDFPINELLDTDLISKIELPSENTESL
X 10 20 30 40 50 60 70
80 90 100 110 120 130 140
VQNSYVPRYDSNGTSEIEEYDVDFNVFFYLHAQKPEGETNISLTSIDTALLESKD-IPFSEFIDTI
TDENVDPVYKQPA--IKKIFTDENTIFQYLYSQTFFLDIRDISLTSFDDALLFSKNKYVSFFSMDYKTA
150 160 170 180 190 200 210
NKPVNAALFIDWISKVIRFTTEATCKSTVDKIDISLIVPVGLALNIIIEAKGNFEAFELLYGVILLE
NKYVEAGLFAGWVKQIVNDFVIEANKSNTMDKIDISLIVPVGLALNIIIEAKGNFEAFELLYGVILLE
150 160 170 180 190 200 210
220 230 240 250 260 270 280
FYPELIPVILVFTKSYSDSVENKKAIAKAINSLIEREAKWKIYIWSNWLTRINTOFNKKQMQQA
FIPPELLIPVAGFLSEYID--NKNKIITIDNALTNRNEKWSMDYGLIVAQWLSTVNTOFFYIKEGMYKA
290 300 310 320 330 340 350
LQNOVDAIKATAYKYNNYTSDEKNRLESEYNNIEELANKYSLAMKNIERFETESSYSLMKLINEAKV
LNQAOALEEIKYRNIYSEKESNINIDF--NDINSKLEGINQADINNFINGCSVSLMKKMIPLAV
360 370 380 390 400 X
GKLKYNHVKSDLLNYILDHRSILGEQTNELSDLVSTLNSIPFELS
EKLLDFDNLKKNLLNYIDENKLYLIGSAEYKSKVNYLKTIMPFDLSIYNTDITILEMENKYNSEIL
360 370 380 390 400 410 420

Copied from 10910186 on 05-05-2004

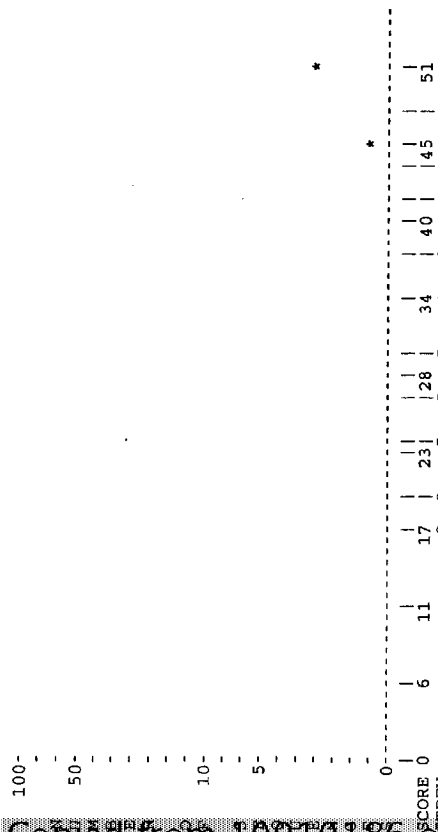
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-31.res made by bobyen on Thu 7 Nov 102 14:50:45-PST.

Query sequence being compared: US-09-910-186A-31 (1-1233)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-31 (1-1233) with:
File: US08123975A.seq



Parameters

Similarity matrix	Unitary	k-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Mean	Median	Standard Deviation
49	45	3.46

Times: CPU 00:00:00.00
Total Elapsed 00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	51	427	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	51	427	0.58	0
3. US-08-123-975A-6	Sequence 6, Application U	1351	45	338	-1.15	0

*** 1 standard deviation below mean ****

1. US-09-910-186A-31 (1-1233)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 51 Optimized Score = 427 Significance = 0.58
Residue Identity = 43% Matches = 518 Mismatches = 599
Gaps = 84 Conservative Substitutions = 0

X 10 20 30 40 50
ATGCCAAATAATACCGGTAAATCTGAACAGTGTATATATTTAAATAT-GAG
CTAAAGTTAACTTCGATCCGATCGACAAGAAT-CAGATCCAGCTGTTCATCTGGAATCTTCCAAATCGAA
140 150 160 170 180 190 200
GATTTATTTTCATAGCTA---ATAAGATAGTTTTCAAAAGATT---TAGCTAAAGCAGAACTATAGC
110 120 130 140 150 160 170 180
GTTATCTGAAGATGCTATCGTATACAACTCTATGTACGAAACTTCTCCACCTCTCTGGATCCGTATC
210 220 230 240 250 260 270 280
ATATATACACAAAT--ATACTATAGAAATATTTTCTATAGATCAGTTGATTTAGTAATGAT--T
190 200 210 220 230 240 250
TAAGCAGTGGCATAGTACCAATGAACACACACACCAATTTACAAATTTTGACGACATAGATATCCCTG
360 370 380 390 400 410 420
TGGAAGTATCTCTGAACTAC--GGTGAATCATCTGGACTCTGGAGGACCTCAGGAATCAACACGCGTG
260 270 280 290 300 310 320 330 340 350
TGATATTAACAATCTGCTTTAAAAAAATTTTGTGATGGAGATAGCCCTTTTGAATATTTACATGCTC
TTGATTTCAATATCTCTGATGATCAACATCTCTGACTACATCAATCG-CTGGATCTCTGTACCATCACC
430 440 450 460 470 480 490
330 340 350 360 370 380 390
AAACATTCCTCTTAATAGAAATCTCAACTACGAATTC---ATTAATGATGCTTTAAGAATAAT
AACAATCGTCTGAATAACTCCAAATCTTACATCAACGGCCGCTGATCGACAGAAACCGATCTCCAACTCG
500 510 520 530 540 550 560
400 410 420 430 440 450
ATAAAGTCTATATCTTTT-----TTTCTACAAC---CTGTGTAAGAAAGCTAAATACAGTTGTAGGTGC
570 580 590 600 610 620 630
GGTAACATCCACGCTTCTAATACATCATGTTCAAACTGGACGTTGTCGACACTCACCAGCTACATCTGG
460 470 480 490 500 510 520
TTCACCTTTTGTAACTG--GGTAAGAGGATTAATAGATGATTTTA-CATCTGAATCCACACAAAAGTAC
ATCAAAATACCTTCAATCTGTTCGACAAAGAACTGAACGAAAGAAATCAAGACCTGTACGACACCCGCTCC
640 650 660 670 680 690 700 710
530 540 550 560 570 580 590
TATAGATAAGTTTCAGATGATCCATATTTTCCCTATA-TAGGAC---CTGCTTTGAATGTAGGAATG
AATTCGATCTCTGAAAGACTTCTGGGTGACTACCTGCATGACGAAACCGGACTACTGATCTGATCTG
720 730 740 750 760 770 780
600 610 620 630 640
AAACAGCTAAAGAA-----ATTTTAAATG-----CTTTTGAATAGGTGGA--GCCGCTAT

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TACGATCCGAAACAAATACGTTGACGTCAACAATGATAGGTATCCGGGTTACATGTACCTGAAAGTCCGGCT
790 800 810 820 830 840 850

650 660 670 680 690 700 710
CTTAAGGAGTTATTTCCAGACTTATTTACTATAGTTGATTTTACATTAAGATCATATGTAGGAAA
|||||
GGTCTGTTATGATACCAACAGTCTACCTGAACTTCCCTGATCCGTTGATACCAATTCATCATCAGAAA
860 870 880 890 900 910 920

720 730 740 750 760 770 780 790
TAAAGGCAATATATATGAGTATCCCAATGCTTTAAGAAAGGGATCAAAATGACAGATATGTATGG
|||||
TACGCTGCTGTTAAGAGCAATATCGTTCCACAAATGATCGGTGATATACATCAATG--TTGATGTTAAGA
930 940 950 960 970 980 990

TTTGATAGTATCCGAGTGGCTCAACGGTTAATCAATTTTATCAATAAAGAAAGAAATGTACAAA---
800 810 820 830 840 850 860
ACAAAGAAATACCG-TCTGGCTACCAATGCTTCTCAGGCTGTTGATAGAAAGATCTTCTGCTCTGGAAATC
1000 1010 1020 1030 1040 1050 1060

GATAAATGATAT---TAACTATGATATAGATATGATATGATATGATATGATATGATATGATATGATATGAT
940 950 960 970 980 990
ATATAAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT
120 130 140 150 160 170 180
CCGAAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT
290 300 310 320 330 340 350

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190 200 210 220 230 240 250
TAGCAGTGGCATGACITTTACCAATGAAACACAGAACCAATTTTACAAATTTTACGACATAGATATCCCTG
|||||
TGAAGATATCTCTGAACTAC--GGTGAATATCTCTGAGCTCTGAGGACACTCAGGAAATCAACAGCTGG
360 370 380 390 400 410 420

260 270 280 290 300 310 320
TGATATTAACAACATCTGCTTTAAAAAAATTTTGTGGAGGAGATAGCCCTTTTGTGAATATTTACATGCTC
|||||
TTGTATCAATACCTCTGAGATGACCAATCTCTGAGTACATCAATCG-CTGGATCTCTGCTTACCATCACC
430 440 450 460 470 480 490

330 340 350 360 370 380 390
AAAATTTCTCTCTTAATATAGAAATCTACAACTAACGAATTC-----ATTAATGATGCTTTTAAAGAAATAT
|||||
GGAACATCCACGCTTCTTAATACATCATGTTCAAACTGGACGTTTGTGCTGACACTCACCGCTACATCTGG
570 580 590 600 610 620 630

500 510 520 530 540 550 560
AACAACTGCTGATTAATCCCAAAATCTACATCAACGCGCTCTGATCGACAGAAACCGATCTCCAACTG
|||||

400 410 420 430 440 450
AATAAGTCTATCTATCTTT-----TTTCTTACAAAC---CTTGTGAAAGCTTAATACAGTTGTAGGTGC
|||||
GGTAACATCCACGCTTCTTAATACATCATGTTCAAACTGGACGTTTGTGCTGACACTCACCGCTACATCTGG
570 580 590 600 610 620 630

460 470 480 490 500 510 520
TTCACTTTTGTAACTG--GGTAAAGAGTAAATAGATGATTTTA-CATCTGATCCACACAAAAGATGAC
|||||
ATCAATATCTTCAATCTGTTCCGACAAAGAACTGAACGAAAGAAATCAAGAGCTGTGTACGACAAACAGTCC
640 650 660 670 680 690 700 710

530 540 550 560 570 580 590
TATAGATAAGTTTCAGATGATCCATATTTTCCCTATA-TAGGAC---CTGCTTTGATGTAGGAATG
|||||
AATTCGCTATCTCTGAAGAGCTTCTGGGTGACTACCTGACGATGACGAAACCGTACTCATGTGTGATGTCG
720 730 740 750 760 770 780

600 610 620 630
AAACAGCTAAAGAAA-----ATTTTAAATG-----CTTTGAAATAGTGGA--CCGCTAT
|||||
TAGATCCGACAAATACGTTGACCTCAACATGATGATAGGTATCCCGGTTTACATGTACCTGAAAGTCCGGCT
790 800 810 820 830 840 850

650 660 670 680 690 700 710
CTTAATGAGTATTTATCCAGAACTTATTTGATCTATAGTTGATTTTATGATATGATATGATATGATAGAAA
|||||
GGTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTTACCGTGGTACCAAAATTCATCATCAAGAAA
860 870 880 890 900 910 920

720 730 740 750 760 770 780 790
TAAAGGCAATATATATGAGTATCCCAATGCTTTAAGAAAGGGATCAAAATGACAGATATGTATGG
|||||
TAGCGCTCTGTTAACAAGGACAAATCGTTCCGACAAATGATCGGTGATACATCAATG--TTGATGTTAAGA
930 940 950 960 970 980 990

800 810 820 830 840 850 860
TTTGATGATATCCGAGTGGCTCTCAACGGTTAATCTACTCAATTTTATCAATTAAGAAAGAAATGTACAA---
|||||
ACAAAGAAATACCG-TCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAGATCTGTCTCTCTGGAATC
1000 1010 1020 1030 1040 1050 1060

--TCTTTAATTAATCAATCAACAGCAATGAAAGAAATAGAGATCAATATAGATATGATATGATAGTAAAGAA
870 880 890 900 910 920 930
CCGACGCTGGTAAATCTGCTGAGTGTGATTAAGA-ATCCCAAGA--ACGACGAGGTATCTACTACAA
1070 1080 1090 1100 1110 1120 1130

940 950 960 970 980 990
GATAAATGATAT---TAACTATGATATAGATATGATATGATATGATATGATATGATATGATATGATATGAT
|||||
TGCAAAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT
1140 1150 1160 1170 1180 1190 1200

530 540 550 560 570 580 590
TATAGATAAGTTTCAGATGATCCATATTTTCCCTATA-TAGGAC---CTGCTTTGATGTAGGAATG
|||||
AATTCGCTATCTCTGAAGAGCTTCTGGGTGACTACCTGACGATGACGAAACCGTACTCATGTGTGATGTCG
720 730 740 750 760 770 780

600 610 620 630
AAACAGCTAAAGAAA-----ATTTTAAATG-----CTTTGAAATAGTGGA--CCGCTAT
|||||
TAGATCCGACAAATACGTTGACCTCAACATGATGATAGGTATCCCGGTTTACATGTACCTGAAAGTCCGGCT
790 800 810 820 830 840 850

650 660 670 680 690 700 710
CTTAATGAGTATTTATCCAGAACTTATTTGATCTATAGTTGATTTTATGATATGATATGATATGATAGAAA
|||||
GGTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTTACCGTGGTACCAAAATTCATCATCAAGAAA
860 870 880 890 900 910 920

720 730 740 750 760 770 780 790
TAAAGGCAATATATATGAGTATCCCAATGCTTTAAGAAAGGGATCAAAATGACAGATATGTATGG
|||||
TAGCGCTCTGTTAACAAGGACAAATCGTTCCGACAAATGATCGGTGATACATCAATG--TTGATGTTAAGA
930 940 950 960 970 980 990

800 810 820 830 840 850 860
TTTGATGATATCCGAGTGGCTCTCAACGGTTAATCTACTCAATTTTATCAATTAAGAAAGAAATGTACAA---
|||||
ACAAAGAAATACCG-TCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAGATCTGTCTCTCTGGAATC
1000 1010 1020 1030 1040 1050 1060

--TCTTTAATTAATCAATCAACAGCAATGAAAGAAATAGAGATCAATATAGATATGATATGATAGTAAAGAA
870 880 890 900 910 920 930
CCGACGCTGGTAAATCTGCTGAGTGTGATTAAGA-ATCCCAAGA--ACGACGAGGTATCTACTACAA
1070 1080 1090 1100 1110 1120 1130

940 950 960 970 980 990
GATAAATGATAT---TAACTATGATATAGATATGATATGATATGATATGATATGATATGATATGATATGAT
|||||
TGCAAAATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT
1140 1150 1160 1170 1180 1190 1200

```

1000 1010 1020 1030 1040 1050 1060
AATAACAATATAGAT-GATTITTTAAACCAATGTTCTATATCATATCTAATCAATAGAAATGATTCATTAG
|||||
|||
GCTAAACGGTTGCTTCCAACTGGTACAATGTCAGATCCGAAGTCTCTCCCACTCTGGGTGTCCTTGG
1210 1220 1230 1240 1250 1260 1270 1280
10070 1080 1090 1100 1110 1120 1130 1140
CTGTAAAAAGTTAAAGACTTTCATGATATCTTAGACAGAGATTTATTGGAGTATATAGATACAATAAGAAC
|||||
GAGTTCA-----TCCCGGTTGATACGGTTGGGGTGAACGTCCGCTCTAAACCCGGGAAAGCTT
1290 1300 1310 1320 1330
1150
TATATTTACTTGAAGAA

```

US-09-910-186A-31 (1-1233)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 45 Optimized Score = 328 Significance = -1.15
Residue Identity = 40% Matches = 367 Mismatches = 501
Gaps = 33 Conservative Substitutions = 0

      350       360       X       370       380       390       400       410
AATATAGAAATCTACAACTAACGAATTCAATAAAT--GATGCTTTTAAAGAAATTAATAAAGTCGTACTACTT
          |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
ATGCCTTTCAACAATAACAATCCGAATCTCGAACAAATATCATCTGAAAC
          X           X       10       20       30       40

```

CTAACGGTGAATCATCTTTCAAAGTGGACGGTGACATCGATCGTACCAGTTTCATCTGGATGAATACATTCT	560	570	580	590	600	610	620
1980	990	1000	1010	1020	1030	1040	
TTAACTTAATCAAAGTATAAATTTAGCATAATAACAATATAGATGATTTTATAACCAATGTTCTTATATACATA	1050	1060	1070	1080	1090	1100	
CTCATCTTCAACACCAAGCTGTCTCAG--TCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGGAATA	630	640	650	660	670	680	690
TTAAATGAA	---	TAGATGATTCCATTAGCTGT	AAAAAG--TTAAAGAC	TTTGATGATATCTTAAATCTTAAAG			
CTGGAAGACATTTCTGGGTATATCCGCTGATGTACACAAAGAAATACTATATGTTCATGTGGTGAACAAGA-	700	710	720	730	740	750	760
1110	1120	1130	1140	1150	1160	1170	1180
AGATTATTTGGAGTATATAGATACAAATGACACTATATTTACTTGATCAAGTAAATATCTTAAATCAAAAGT							
ACTCTTACATCAAATCGAAGAAAGACTCTCCGGTGTGGTGAAATCCTGACCTGTTCCAAATATCAACACGAGACT	770	780	790	800	810	820	830
840							
1190	1200	1210	1220	1230	x		
AAATAGACACCTAAAAA-----GACAGTATACCAATTTGATCTTTCACATATACCTAA							
CTAAATACATCAACTACCGCGGACCTGTACATCGGTGAAAGATTTCATCATCCGTCGGCAAAATCAACCTCTCAGT	850	860	870	880	890	900	910
CCATC							

US-09-910-186A-31' (1-1233)
US-08-123-975A-1 Sequence 1, Application US/08123975A


```
150 160 170 180 190 200 210
ERANTVVGASLVNWKGVDDFTSESTQKIDKVSIVSIIPYIGPALNVGNENKFAEIGGAAI
: : : : :
NNSKIYINGRLIDQRPISNLGNIHANNIMEKLCGRDTHRYIWKYFNLFDKELNEKEIKDLVDNOSNGI
150 160 170 180 190 200 210
220 230 240 250 260 270 280
LMFEPDELIVPIVGFTELESYVGNKGHIIMTISNALKKRDQKWTMDTGLIVSQWLSVNTQFYTIKERMVNA
: : : : :
LKDFWGDYLOYDKPYMLNLDPNK---YVDVNVVGIKGYMYLKGPRGSMVTNNIYLNSSLYRGRTFIIRKY
220 230 240 250 260 270 280
290 300 310 320 330 340 350 360
LNNQSAIEKIIEDQYNYSEEDKNINIDNDDFKLNQINAINNIDDFINQCSISYILMNRKPLAVKK
ASGNKDNIVNRNDRYIINVVKNEYRATNASAGVEKIISALEIPDVGNLSQVYVVKSKNDQGITNKCKM
290 300 310 320 330 340 350
370 380 390 400 410
LKDFDNLKRDLEVIDTGNELYLLDEVNLLKSKVNRHLKDSIPFDLSLYT
NLQDNNGNDIGIGIHFQFNHIAKLYASWYNRQIERSSTLGCSEWEPYVDGKGWGERPL
360 370 380 390 400 410
US-09-910-186A-32 (1-410)
US-08-123-975A-5 Sequence 5, Application US/08123975A
```

Initial Score = 14 Optimized Score = 132 Significance = -0.60
Residue Identity = 11% Matches = 32 Mismatches = 239
Gaps = 1 Conservative Substitutions = 18

```
110 120 130 140 150 160 170
DSLFEYLHAQTSPNENLQNLNSLDALRNKNKYVTFSTNLVEKANTVVGASLVNWKGVDDFTSEST
: : : : :
FNKYNSEILNNIILNRYKDNLDLDSOYGAKVEYDGVDELNDKNQKFLRSS
X 10 20 30 40 50
```

```
180 190 200 210 220 230 240
QKSTIDKVSIVSIIPYIGPALNVGNENKFAEIGGAAILMEFIPELIPIVGFTELESYVGNKGHI
: : : : :
ANSKIRVTQNIIFNSVFLDFSVSFWRIPKPKNDGIGNIHNHYTIINCMKNNSGKISIRGNRIIWTLI
60 70 80 90 100 110 120
```

```
250 260 270 280 290 300 310
IMTISNALKKRDQKWTMDYGLIVSQWLSVNTQFYTIKERMYNALNNQSAIEKIIEDQYNYSEEDKNIN
: : : : :
DINGKTKSVFFEYFNIREDISVINRWFFVTIITNNLN-NAKIYINGKLESNTDIKDIREVIANGSEIIFKLDGD
130 140 150 160 170 180 190
```

```
320 330 340 350 360 370 380
IDFNDIDFKLNSINLAINNIDDFINQCSISYILMNRMPLAVKKLKDFFDNLKRDLEVIDTGNELYLLDEVN
: : : : :
IDRTQFIWMKYFSIFNTLSOSNIEERYKIQSYEYLKDFWGNPLMYNKNEYMFNAGKNNSYIKLKKDSPVG
200 210 220 230 240 250 260
```

```
390 400 X
ILASKVNRHLKDSIPFDLSLYT
: : :
EILTRSKYQNQNSKYINRYDLIYIGERKEFIIRKNSQSINDDIV
270 280 290 300
```


70 80 90 100 110 120 130 140
 AAAGACAACTCTAATCCTGGACATCGGTTACGAAACAACAATAATTCATCGACATCTCTGGTATGGTCTTAC
 ATCAATACCTCCATCCTGACACCTCGGCTAGCAATCCAAATCACTGATCGACCTGTCTCGCTAGCTCTGCCAA
 150 160 170 180 190 200 210
 ATCTCTATCAACGGGTGACGCTACATCTACTTACTTAACCGCAACCACTCGGTATCTATCTTCTAAACCG
 ATCAACATCGGTCTCTAAAGTTAACTTCGATCCGATCGATCGACAAGAAATCAGATCCAGCTCTTCAATCTGGAACT
 220 230 240 250 260 270 280
 TCTGAAGTTAAACATCGCTCAGACAACGACATCTCTAAGCGGTCTGTTACAGAACTTCTCTATCTCTTTTC
 TCCAAATTCGAAGTTATCCTGAAGAATGTTATCGTATACAACATCTATGTAGCAAACTTCTCCACCTCTTC
 290 300 310 320 330 340 350
 TGGGTCTGATCCCGAATACTCTCAACAAGTTAACTTCAACAACGAATACACTATCATCGACTGCATCGCTCGT
 TGGATCCGTTATCCCGAATACTCTCAACTCCATCTCTGAAACAATGAATACCACTCATCACTGATGAT---G
 360 370 380 390 400 410 420
 AACACAACATCTCGGTGGAATACTCTCTGAACATCAACAATAATCATCTGCACCTCGAGCACACTGCTGGT
 GAACAACATCTCGGTGGAAGATCTCTGAACTACGGGTAATCATCTGACCTTCGAGACACTCAGAA
 330 340 350 360 370 380 390 400 410
 AACACAACGAGTGTGTTTCAACTACATCAGATGATCTCTCTGACTACATTAATAATGATCTTC
 ATCAACACGCGTGTGTTTCAATACTCTCAGATGATCAACATCTCTGACTATCATCAATCGGTGATCTTC
 420 430 440 450 460 470 480 490 500
 GTTACTATCACTAACACCGCTCTGGTAACTCTGCTATCTACATCAACGGTAACTGATCGATGAAATACT
 GTTACCATCAACAATCTGTTGAATACTCCAAATATACATCAACGGCGCTCTGATCGACCAAGAACCG
 510 520 530 540 550 560 570
 ATCTCTAACCTCGGTGACATCCAGTGTCTGACACATCTGTTCAAAATCGTGTTCAGACGAC---G
 ATCTCCAACTCGGTGTAATCCACCGTCTTAATTAACATCATGTTTCAACTGGACGGTGTCTGTGACACTCAC
 580 590 600 610 620 630 640
 CGTACGTTGTTATCCGTTACTTCAAAAGTTTTCGACATGAACTGGGTGAAACTGAAATCGAACTCTGTAC
 CGCTACATCTGGATCAAAATCTTCAATCTGTTCGACAAGACTGACGAAAAAGAAATCAAGACCTGTAC
 650 660 670 680 690 700 710
 TCTGACGAACCGGACCGTCTATCTCTGAAGACTTCTGGGTAACTACTGCTGTACACAAACGTTACTTAC
 GACAACCAAGTCCCAATCTCGGTATCTCTGAAGACTTCTGGGTGACTACTGCTGACTGACGACAAACCGTACTAC
 720 730 740 750 760 770 780
 790 800 810 820 830 840
 CTGCTGAACCGTCTCCGACTGCAAAAT--CTATCACTCAGAACTCTAACT-----TCTGCAATCATC
 ATGCTGTAATCTGTACGATCCGGAACAAATAGGTTGAGCTGCAACAATGTAGGTATCCCGCGTTTACATGACTCG
 850 860 870 880 890 900
 AACCAGCAGCGGTGTTTATCAGAAACCTTAATATCTTCTTAACCACTCGCTCTGTACACTGTTGTGAAGTT

```
Initial Score      = 557 Optimized Score = 788 Significance = 0.59
Residue Identity = 61% Matches      = 829 Mismatches = 451
Gaps              = 71 Conservative Substitutions = 0
```

10 20 30 40 50 60
GAATTCAGGATGCTTTAACTAACGACAAAATCCTGATCCTGT---ACTTCAACCAACTGTACAAAAAATC

```

AAAGTCCCGGTGTTCTGTTATGACTACCAACATCTACCTGAACCTCTCCCTGTACCGTGGTACCAAAATTC
850 860 870 880 890 900 910

920 930 940 950 960 970 980 990
ATCATCCGTAAACAGGTTTACTGACATCTCTAAACACTGACAACTGGTACGTAACAGCGCTGCTTAC
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
ATCATCAAGAAATACGCGTCT-----GGTAAAGGACAAATATGTTTCGCAACAATGATCGTGTATAC
920 930 940 950 960 970

1000 1010 1020 1030 1040 1050 1060
ATCAACGGTTGACCGGTGACGTTGAATACCGTCTGTAGCTGACATCTCTATCGTAAACCGGAAACATTC
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
ATCAATGTTGTGTTAAGAACAAAGAAATACCGTGTGGTACCAATGCTTCACGCGTGGTGTAGAAAGATC
980 990 1000 1010 1020 1030 1040

1070 1080 1090 1100 1110 1120
ATCAAACTGATCGGTACTTCACTCACTCACTCTCTGGTCCAGATCATCGTWTGACATC-----
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
TTGCTGCTCTGGAATCCCGGACGTTGGTAA---TCGTCTCAGGTAGTGTGTAATGAATCCCAAGAACGAC
1050 1060 1070 1080 1090 1100 1110

-----GATCGGTAAACAGTGCATCTGAACCTCCAGAACAAACAGCGTGGTAACTGCTGCTGGTTC
1130 1140 1150 1160 1170 1180 1190
CAGGCTATCACTAAACAATGGAATGATCTCGAGGACAAATGGTAAGTATCGGTTTCATCGGTTTC
1120 1130 1140 1150 1160 1170 1180 1190

1200 1210 1220 1230 1240 1250 1260
CACTCTAAACAAAC-----CTGGTGTGTTCTTATGATGATGATCAACAACTCCGTAACAACTTCT
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
CACCAGTTCACAAATATCGCTAACTGTTGCTTCCAACTGCTACAACTCGTACAGTGAAGTTCCTCTGCG
1200 1210 1220 1230 1240 1250 1260

1260 1270 1280 1290 1300 1310 1320 1330
TCTAACGGTGTCTTGGTCTTCACTCTAAGAACACAGGTTGTCAGGA-----AAACTAAGAT
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
ACTCTGGTTCCTTGGGAGTTCAACCGGTTGATGAGCGTGGGTGAACGTTCCGCTGTAACCCCGGAAA
1270 1280 1290 1300 1310 1320 1330

X
TC
GCTT
X
US-09-910-186a-33 (1-1314)
US-08-123-975A-6 Sequence 6, Application US/08123975A
Initial Score = 487 Optimized Score = 678 Significance = -1.14
Positive Identity = 54% Matches = 740 Mismatches = 520
Conservative Substitutions = 0
20 30 40 50 60 70 80 90
CTAAGCAAAATCCTGATCTGATCTCAACAACTGTACAAAATCAAGAACTATCTCCCTGGACA
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
ATGGCTTCAACAAATACAAATCCGAAATCCCTGAAATGAAATATCATCTCCGTAACCC
X 10 20 30 40 50
100 110 120 130 140 150 160
TGGTTCGGAACAAACAAATCATGACATCTCTGGCTATGTTCTACATCTCTATCAACAGGTGAGTCT
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
TGGTTCACAAAGCAACAACTCTGATCGTCTGTGTTACGGTGTAAAGTTGAAGTATACGAGCGGTGG
60 70 80 90 100 110 120

170 180 190 200 210 220 230
ACATCTACTCTACTAACCGCAACGCTCTGCTGATCTCTCTTAAACCGCTGTAAGTAAACATCGCTCACA
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AACT-----GAATGACAAAGAACCACTCAACTGACCTCTCTCCGCTCACTCAAGATCCCGTGTACACGA
130 140 150 160 170 180 190

240 250 260 270 280 290 300
ACACGACATCATCTACACGGTCTGTACCAAGAACTCTCTATCTCTTCTGGTTCGTATCCCGAAATACT
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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ATCAGAACATCATCTCTCACTCCGTAATTCCTGGACTCTCTGTTCTCTGGATCCGTAATCCGAATACA
200 210 220 230 240 250 260

310 320 330 340 350 360 370
TCAACAAAGTTTAACTCGA-----ACAACGATACACTATCATCGACTGCATCGTACACAACTCTG
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AGAACGCGGTATCCAGAAATTACATCCCAATGATATACACCATCATCAACTGCAT---GAAGATAACTCTG
270 280 290 300 310 320 330

380 390 400 410 420 430 440
GTGGAAATCTCTGTGAACCTACAAACAAATCACTGTGACTCTGAGGACACTGCTGTACAAACCGAAAC
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
GTGGAAATCTCTCCATCCCGGTACCTGATCATCTGACTCTGATCATCAACGCTAGACGAAATCTG
340 350 360 370 380 390 400

450 460 470 480 490 500 510
TGGTTTCAACTACACTGATGATCTCTATCTCTGACTACATTAATTAATGGATCTCTGTTACTATCATA
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
TATCTTCAATACAACTCCGTAACCTGTAATACATCAATCAATCGTCTCTGTTACCATCACA
410 420 430 440 450 460 470

520 530 540 550 560 570 580
ACAAACGCTCTGGTAACTCTCTATCTACATCAACGCTAACTGATCGATGAAATCTATCTCTACCTGG
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
ATTAAC---CTGAACATGCTAAATCTACATCAACGCTAACTGGAATCTAATCCGACATCAAGACATCC
480 490 500 510 520 530 540

590 600 610 620 630 640 650
GTGACATCCACGTTCTGTAACATCTCTGTTCAAAATGTTGGTTGCAACGA---CACGCGTACGTTGGTA
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
GTGAATCTCTGCTACGCTGGAATCACTTCAAACTGGACGGTGACATCGATCTACCCAGTTTCACTGGA
550 560 570 580 590 600 610

660 670 680 690 700 710 720
TCCGTTACTTCAAGTTTTCGACACTGACTGGTAAACTGAAATGAAATCTGTACTCTGACGACCGG
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
TGAATACCTCTCCATCTTCAACGCGAACTGTCTCAGTCCAAATATCGAAGACGGTACAGATCCAGTCTT
620 630 640 650 660 670 680

730 740 750 760 770 780 790
ACCCGCTTCTCTGAAAGACTTCTGGGTAACTACTGCTGTACAAACAACTGACTACTGCTGTAACCGTC
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
ACTCCGAATACCTGAAAGACTTCTGGGTAACTCCGCTGATGTACAAAGAACTATATGTTTCAATGCTG
690 700 710 720 730 740 750 760

800 810 820 830 840 850 860
TCCGGACTGACAAATCTACTCAGAACTCTAACT-TCCTGAACATCAA--CCAGACGGTGGTGT---
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
GTAACGAAGACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAATCTCTGCTCTCCAAATACA
770 780 790 800 810 820 830

870 880 890 900 910 920 930
ATCAGAACTTATATCTTCTTACACTCTGCTGACACTGGTGTGAACTATCATCCGTAACAAACGGTT
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
ACCAGAACTTAAATACATCAACTACCGGACCTGTACATCGTGAAGAACTCATCATCCGTCGAA---AT
840 850 860 870 880 890 900

940 950 960 970 980 990 1000
CTACTGACTCTTAACTGACAACTCTGCTAGTAAACAAACGCTGGCTTACATCAACGTTGTGACGGT
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
CTAATCTGCTCCATCATGATGACATCTGATGTAAGAAAGCTTACATCTACCTGGACTTCTTCAACCTGA
910 920 930 940 950 960 970

1010 1020 1030 1040 1050 1060 1070 1080
ACGTTGAATACCGTGTGAGTACATCTCTATCGTAAACCGGAAACAAATCATCAACGTTGCTGCTACT
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
ATCAGAAATGGCTGTATACACCTCAAGTACTTCAAGAAAGAAAGAAAGCTTTTCTGCTGCTCGATCT
980 990 1000 1010 1020 1030 1040

1090 1100 1110 1120 1130 1140 1150
CTAATCTTAACT-AACTCTCTGCTGATCAGATCATCTGTTGACTCGATCGGTAAC--AACTGCACTATGACT
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Copied from 10910186 on 05-05-2004

TTCAAGAAAGATGAAGAAATCTACTGACGAAATCGGTCTGATCCACCGTTTCTAGCAATCTGAT-AT
1130 1140 1150 1160 1170 1180 1190
1170 1180 1190 1200 1210 1220
AGAGATGTTAGAACCATACCCAGAGATGTCGAT-----GATTTGTTGTTTTCGTACCCA---TGTC
CGTATTCGAAGATACAAAGACATCTTCTGCAATCTCCAAATGCTACCTGAAGGAAGTTAAACGCAACCGTA
1200 1210 1220 1230 1240 1250 1260
1230 1240 1250 1260 1270 1280 1290
CAGGATAGAGTTGCTTTGATTTTGTGACAGTTTGTGAAGTACAGGATCAGGATTTGTCGTTAGTGTGA
CAACCTGAAGCTGSETTGCAATTGGCAGTTCA--TCCCGAAGACGAGGTTGGACCGAATAGTAACTCT
1270 1280 1290 1300 1310 1320 1330
1300 1310 X
AGACATCGTGAATC
AGAGTGGAGGCGCTGCAG
1340 1350

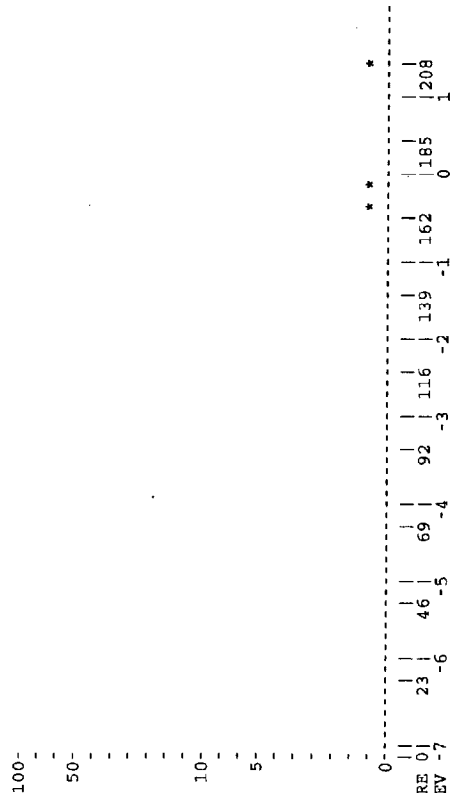
> O <
O I O Intelligence
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-34.res made by bobryen on Thu 7 Nov 102 14:38:25-PST.

Query sequence being compared:US-09-910-186A-34 (1-432)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-34 (1-432) with:
File : US08123975A.pep



PARAMETERS
Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 16%
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 432
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

SEARCH STATISTICS
Scores: Mean Median Standard Deviation
181 165 23.64
Times: CPU 00:00:00.00
Total Elapsed 00:00:00.00

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Score Init. Opt.

1. US-08-123-975A-2 Sequence 2, Application US/08123975A
**** 1 standard deviation above mean ****
2. US-08-123-975A-3 Sequence 3, Application US/08123975A
**** 0 standard deviation from mean ****
3. US-08-123-975A-5 Sequence 5, Application US/08123975A
**** 0 standard deviation from mean ****

1. US-09-910-186A-34 (1-432)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score = 208 Optimized Score = 264 Significance = 1.14
Residue Identity = 35% Matches = 163 Mismatches = 231
Gaps = 28 Conservative Substitutions = 33

X 10 20 30 40 50
MSYTDKILLYFNKLYKKIKDMSILDMRYENKFKIDISGYGNSINISGVY
AYEKSVMKYLKTIKMPDLISYITDIEMFNKYNSEILNIIILNRYKNDLISGYGAKVEYDGYE
380 390 400 410 420 430 440 450
IYSTNRNOFGIYSSKPEVNIAQNNDIYNGRYQNFISFVWRIPKYNKV---NINNEYTIDICIRNNSS
L--NDRNQKLTSSANSKIRVTONQNIENSFLDFSVFWRIPKYNKNDGIONYHNEYTIINCMK--NSG
460 470 480 490 500 510 520
WKISLWYKIIWTLQDTAGNKKLVFNQYQMSISDYINKLWFLVITNRLGNSIYINGNLIDEKSIENLG
WKISIRGNRIIWLIDINGTKSVPEYNIREDISEYINRWFVITNN--LNNAKIYINGKLESNTDIDIR
530 540 550 560 570 580 590
200 210 220 230 240 250 260
DIIVSNILFIYKQND--TRYGIRYKVFDTLQKTEIETILYSDPDPSPILKDFWNTLYNRYLNL
EVZANGEIIFKLDGDDIDRQFIWVKYFISFNTLSQSLNLEERYKIQSYSEYKDFWGNPLMYNKEYYFNAG
600 610 620 630 640 650 660
270 280 290 300 310 320 330
RTDKSITQNSNF--LNINQORGYQKPNFISNTRLYTIGVEIIRKNGSDISNTDNFVKNDLAINVVDROV
NKNSYIKLAKDSPVGEILTRSKYQNSKYINRDLVIGKFTIRKNSQSINDDIVRKYEDYVLDENLQ
670 680 690 700 710 720 730
340 350 360 370 380 390
EYRLYADISIAPEKIIKILRTSNNSNLSGQIIVMD-----SIGNNCTMNFQNNNGNIGLGFH-----
ENRWYTKYFKKEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKDEESTDEIGLIGHRYFESGI
740 750 760 770 780 790 800
400 410 420 X
-----SNNLVASWYNNIRKN--TSSNGCFWFSFKHGWQEN
VFEEYKDYFCISKWLKVEKRPYNKLGKCNMQFIPKDEGWTE
810 820 830 840 850

2. US-09-910-186A-34 (1-432)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score = 171 Optimized Score = 296 Significance = -0.42
Residue Identity = 49% Matches = 205 Mismatches = 168
Gaps = 17 Conservative Substitutions = 27

10 20 30 40 50 60 70 80
LILYFNKLYKKIKDMSILDMRYENKFKIDISGYGNSINISGVYITNRYQFGIYSSKPEVNIAQNNDII
RYESNHLIDLSRYASKINIGSKVNFDPIDKIQIOLFNLESSKIEVILKNAIV
X 10 20 30 40 50

```

100 110 120 130 140 150
YNGRYONFISFWIRIPKYNKVLNNEYTTIDCIRNNNSGKISLNYKIIWTLQDTAGNKKLVNTYOM
110 120 130 140 150
YNSMTNESTFWIRIPKYNFISLNEYTIINC-ENNSGKVSINYEELIWTLODTEIKQVVFVRYSQM
160 170 180 190 200 210 220
ISISDIYINKWIFVTITNRLNLSRIYINGNLIDEKISINLGDHVSNDILFKIVGNDT-RYVGIRYKVED
130 140 150 160 170 180 190
INISDIYINRWIFVTITNRLNLSRIYINGNLIDQKPSINLGHASNNIMEKLDGCDTHRYWIKYFLNFD
230 240 250 260 270 280 290
TELGTETETIYSDEPPSILKDFWGNLYLLNRYKRYLLNLRDTSKITSQNS-NNFLINQOQVYQKPN
200 210 220 230 240 250 260
KELNEKEIKDLYDNQNSGILKDFWGDYLDKPYMLNLYDNKYVDVNNVGIYRGYMLKGRGSMVTNI
300 310 320 330 340 350 360
PSNTFLYTGVEVIRKKGSTDSITDNFVRKNDLAINVVDROVEYRLYADISIAKPEKIIKIRTSNSNS
370 380 390 400 410 420
LGQIIVM----DSIGNCTMNFONNGNIGLGFHS-----NNLVASSWYNNIRKNTSSNGCFWFSFISKEH
430 X
GWOEN
GGERPL
410 X

```

```

280 290 300 310 320 330 340
360 370 380 390
RTSSNNLSLQGIIVMD-----SIGNNCTMNFONNGNIGLGFH-----SNNLVASSWYNNIR
350 360 370 380 390 400 410
PISDSDEFYNTIQIKEYDEQPTYSQOLLFKKDEESTDEIGLIGHRFYESGIVFEYKDYFCISKWYLKEV
420 430
KN--TSSNGCFWFSFISKEHGWQEN
420 430
RKPNLXLGCNMQFIPKDEGWTE
420 430 X

```

US-09-910-186A-34 (1-432)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 164 Optimized Score = 256 Significance = -0.72
Residue Identity = 35% Matches = 156 Mismatches = 226
Gaps = 28 Conservative Substitutions = 33

```

10 X 20 30 40 50 60 70
MSYNDKILILYFNKLYKKIKDSIIDMYENKFKIDISGYGNSISNGDVYIYSTNENQGIYSSKPEVY
110 120 130 140
FNKYNSELNLLNLYKONNLDLSGYKAVEYDGVEL--NDRNQFALTSSANSKIR
X 10 20 30 40 50
80 90 100 110 120 130 140
IAQNDIYNGRYONFISFWIRIPKYNKVLNNEYTTIDCIRNNNSGKISLNYKIIWTLQDTAGN
130 140 150 160 170 180 190 200
VTQONLIFNSVFLDFSVFWIRIPKYNKNDGIONYIHNEYTIINCWK-NNSGWKISIRGNRIIWTLDINGK
60 70 80 90 100 110 120
150 160 170 180 190 200 210
NQKLVNTQIMISDIYINKWIFVTITNRLNLSRIYINGNLIDEKISINLGDHVSNDILFKIVGND-TR
130 140 150 160 170 180 190 200
TKSVFEYNIREDISYINRWIFVTITN-LNNAKIYINGKLESNTDKIDREVIANGELIFKLDGDDIDRTO
130 140 150 160 170 180 190 200
FINKYFISITBELSOSNEERYKIQSYSEYLDKDFGNPLMYNKEYMFGNKNKSYTKKKDSFVGEILTR
210 220 230 240 250 260 270
290 300 310 320 330 340 350
GVYQKPIFNTFLYTGVEVIRKKGSTDSITDNFVRKNDLAINVVDROVEYRLYADISIAKPEKIIKI
SKYNQSKYINRDLYIGKEFIIRKKSNSQSDINDIVRKEDYIYLDFFNLNQEWVRVITYKYFKKEEKEFLA

```